

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:40 : Search time 30 seconds
(without alignments)
1965.226 Million cell updates/sec

Title: US-09-787-083-2

Perfect score: 442

Sequence: 1 MKVSLSTLTLSTLSCFALLA.....YNHEATSPFGVGLMDNMWGL 442

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq.101002.*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	442	100.0	442	21	AAV85268	BASB034 amino acid
2	337	74.0	442	21	AAV85271	BASB034 amino acid
3	289	65.4	289	23	AAO17569	M catarrhalis MCA1
4	224	50.7	442	21	AAV85269	BASB034 amino acid
5	224	50.7	442	21	AAV85270	BASB034 amino acid
6	9	2.0	255	22	ABG18034	Novel human diagno
7	9	2.0	370	21	AAV75156	Neisseria gonorrhoe
8	9	2.0	370	21	AAV75157	Neisseria meningit
9	9	2.0	370	21	AAV75158	Neisseria meningit
10	9	2.0	374	21	AAV70629	Neisseria meningit

11	9	2.0	375	21	AAV70628	Neisseria meningit
12	8	1.8	278	21	AAG11137	Arabidopsis thalia
13	8	1.8	283	21	AAG11136	Arabidopsis thalia
14	8	1.8	299	21	AAG11135	Arabidopsis thalia
15	16	1.6	15	15	AAV852127	Mouse light chain
16	15	1.6	33	22	AAV76069	Rat alpha tubulin
17	17	1.6	50	21	AAV79483	Arabidopsis thalia
18	18	1.6	64	21	AAV063322	Human cardiovacu
19	19	1.6	75	22	AAV222239	Human secreted pro
20	20	1.6	82	21	AAV01488	Human polypeptide
21	21	1.6	88	22	AAO03041	Arabidopsis thalia
22	22	1.6	106	21	AAV07608	Arabidopsis thalia
23	23	1.6	106	21	AAV51952	Arabidopsis thalia
24	24	1.6	108	21	AAV37811	Arabidopsis thalia
25	25	1.6	110	22	AAO03010	Human polypeptide
26	26	1.6	114	22	AAV53952	Propionibacterium
27	27	1.6	114	22	AAO02870	Human polypeptide
28	28	1.6	116	21	AAV87313	Human signal pepti
29	29	1.6	116	23	ABG65204	Human albumin fusi
30	30	1.6	116	23	ABG65205	Human albumin fusi
31	31	1.6	116	23	ABG65206	Human albumin fusi
32	32	1.6	116	23	AAU91093	Human secreted pro
33	33	1.6	116	23	AAU91120	Human secreted pro
34	34	1.6	116	23	AAU91121	Human secreted pro
35	35	1.6	133	22	ABG27556	Novel human diagno
36	36	1.6	136	21	AAV37810	Arabidopsis thalia
37	37	1.6	157	21	AAV29867	Arabidopsis thalia
38	38	1.6	158	21	AAV79176	Arabidopsis thalia
39	39	1.6	162	23	ABP42371	Haematopoietic ste
40	40	1.6	169	20	AAV34661	Chlamydia pneumoni
41	41	1.6	181	21	AAV37809	Arabidopsis thalia
42	42	1.6	181	23	ABP42926	Human ovarian anti
43	43	1.6	186	21	AAV07607	Arabidopsis thalia
44	44	1.6	186	21	AAV51951	Arabidopsis thalia
45	45	1.6	188	21	AAV51950	Arabidopsis thalia

ALIGNMENTS

```

RESULT 1
ID AAV85268 standard; Protein; 442 AA.
XX
AC AAV85268;
XX
DT 29-JUN-2000 (first entry)
XX
DE BASB034 amino acid sequence #1.
XX
KW Moraxella catarrhalis infection; BASB034; diagnosis; staging;
KW vaccine; bacteriostatic; treatment; prevention; otitis media;
KW sinusitis; nosocomial infection; invasive disease; chronic otitis media;
KW hearing loss; antibacterial drug.
XX
OS Moraxella catarrhalis.
XX
PN WO200015802-A1.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-EP06781.
XX
PR 14-SEP-1998; 98GB-0020002.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Ruella J.
XX
DR WPI; 2000-271440/23.
XX
N-PDB; AAA10700.
XX
PT Novel BASB034 polynucleotides and polypeptides from Moraxella

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PT catarrhalls used to prepare vaccines against bacterial infections
XX
XX Claim 3; Fig 2; 106pp; English.
XX
CC This sequence represents a Moraxella catarrhalls BASB034 polypeptide from
CC strain Mc2931 (ATCC 43617). The invention relates to BASB034 polypeptides
CC from M. catarrhalls strains Mc2931, Mc2908, Mc2913 and Mc2969. The
CC BASB034 polynucleotides and polypeptides may be employed as research
CC reagents and material for the discovery of treatments and diagnostics for
CC diseases, particularly human diseases. They are particularly used to
CC diagnose and treat M. catarrhalls infections. They can be used for
CC diagnosis of disease, staging of disease, or determining response of an
CC infectious organism to drugs. The polynucleotides may be used as a source
CC for hybridization probes, and for screening of genetic mutations,
CC serotype, organism or strain identification, identification of mutations
CC in BASB034 sequences, and as components of arrays which are useful for
CC diagnostic and prognostic purposes. The polypeptides can be used to
CC produce antibodies. The polypeptides can also be used in vaccine
CC formulations, and to identify agonists and antagonists. The polypeptides,
CC antibodies, agonists and antagonists (which are bacteriostatic) are used
CC for the treatment and prevention of diseases such as otitis media in
CC infants and children, pneumonia in elderlies, sinusitis, nosocomial
CC infections and invasive diseases, and chronic otitis media with hearing
CC loss. The polypeptides, agonists and antagonists are also used for
CC screening of antibacterial drugs. The BASB034 products of the invention
CC can be used screen for new antibacterial compounds that may target
CC resistant bacteria.
XX
XX Sequence 442 AA:
SQ
Query Match 100.0%; Score 442; DB 21; Length 442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MKVSLTLTLSTLSCAIIAIOAOAVPNPAVDEVRSNDGONELPIDVQSATQSA 60
DB 1 MKVSLTLTLSTLSCAIIAIOAOAVPNPAVDEVRSNDGONELPIDVQSATQSA 60
OY 61 SDTANPLDEHEBELYTTALENTKMLINCSALNODIMRLACYDTLVHGETPAVTKTKRSI 120
DB 61 SDTANPLDEHEBELYTTALENTKMLINCSALNODIMRLACYDTLVHGETPAVTKTKRSI 120
OY 121 RLDDETWTQIKKRPQYIYQETTDPIFLMGNEKGMILTKKAKOLEYAKOFTPLSLSDLD 180
DB 121 RLDDETWTQIKKRPQYIYQETTDPIFLMGNEKGMILTKKAKOLEYAKOFTPLSLSDLD 180
OY 121 RLDDETWTQIKKRPQYIYQETTDPIFLMGNEKGMILTKKAKOLEYAKOFTPLSLSDLD 180
DB 121 RLDDETWTQIKKRPQYIYQETTDPIFLMGNEKGMILTKKAKOLEYAKOFTPLSLSDLD 180
OY 181 RNNTPLMSSRPNNPNTVLPFLMGKPNRSPNPSHEAKDPTNEFPAPELKFPQVSVKVA 240
DB 181 RNNTPLMSSRPNNPNTVLPFLMGKPNRSPNPSHEAKDPTNEFPAPELKFPQVSVKVA 240
OY 241 AEDLMGTDSDLMFGYQOQSHWQJFNCKNSRPFVNDYQPEIFLTQPVYSDLPMDGKVRMI 300
DB 241 AEDLMGTDSDLMFGYQOQSHWQJFNCKNSRPFVNDYQPEIFLTQPVYSDLPMDGKVRMI 300
OY 241 AEDLMGTDSDLMFGYQOQSHWQJFNCKNSRPFVNDYQPEIFLTQPVYSDLPMDGKVRMI 300
DB 241 AEDLMGTDSDLMFGYQOQSHWQJFNCKNSRPFVNDYQPEIFLTQPVYSDLPMDGKVRMI 300
OY 301 GKGAVHNSGSESKLSRSNNRAYIAGMEKMLTVMPTMGRIFKSGSGSQPDNDNDIID 360
DB 301 GKGAVHNSGSESKLSRSNNRAYIAGMEKMLTVMPTMGRIFKSGSGSQPDNDNDIID 360
OY 361 YGCGVGRFLYOLENKSNTSGTVRYNPRSGKALODYVPLGKISGYSQIQIGYGOSL 420
DB 361 YGCGVGRFLYOLENKSNTSGTVRYNPRSGKALODYVPLGKISGYSQIQIGYGOSL 420
OY 421 IDYNHEATSFVGGLMLNDMMGL 442
DB 421 IDYNHEATSFVGGLMLNDMMGL 442

RESULT 2
ID AAY85271
XX AAY85271 standard; Protein; 442 AA.
XX
XX AAY85271;
XX

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DT 29-JUN-2000 (first entry)
XX
XX BASB034 amino acid sequence #4.
DE
XX Moraxella catarrhalls infection; BASB034; diagnosis; staging;
XX vaccine; bacteriostatic; treatment; prevention; otitis media; pneumonia;
XX sinusitis; nosocomial infection; invasive disease; chronic otitis media;
XX hearing loss; antibacterial drug.
XX
XX Moraxella catarrhalls.
OS
XX WO200015802-A1.
XX
XX 23-MAR-2000.
XX
XX 14-SEP-1999; 99WO-EP06781.
XX
XX 14-SEP-1998; 98GB-0020002.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Ruelle J;
XX
XX WPI; 2000-271440/23.
XX
XX N-PSDB; AAA10703.
XX
XX Novel BASB034 polynucleotides and polypeptides from Moraxella
XX catarrhalls used to prepare vaccines against bacterial infections
XX
XX Claim 3; Page 69; 106pp; English.
XX
XX This sequence represents a Moraxella catarrhalls BASB034 polypeptide from
XX strain Mc2969. The invention relates to BASB034 polypeptides from
XX M. catarrhalls strains Mc2931, Mc2908, Mc2913 and Mc2969. The BASB034
XX polynucleotides and polypeptides may be employed as research reagents and
XX material for the discovery of treatments and diagnostics for diseases,
XX particularly human diseases. They are particularly used to diagnose and
XX treat M. catarrhalls infections. They can be used for diagnosis of
XX disease, staging of disease, or determining response of an infectious
XX organism to drugs. The polynucleotides may be used as a source for
XX hybridization probes, and for screening of genetic mutations, serotype,
XX organism or strain identification, identification of mutations in BASB034
XX sequences, and as components of arrays which are useful for diagnostic
XX and prognostic purposes. The polypeptides can be used to produce
XX antibodies. The polypeptides can also be used in vaccine formulations,
XX and to identify agonists and antagonists. The polypeptides, antibodies,
XX agonists and antagonists (which are bacteriostatic) are used for the
XX treatment and prevention of diseases such as otitis media in infants and
XX children, pneumonia in elderlies, sinusitis, nosocomial infections and
XX invasive diseases, and chronic otitis media with hearing loss. The
XX polypeptides, agonists and antagonists are also used for screening of
XX antibacterial drugs. The BASB034 products of the invention can be used
XX screen for new antibacterial compounds that may target resistant
XX bacteria.
XX
XX Sequence 442 AA:
SQ
Query Match 74.0%; Score 327; DB 21; Length 442;
Best Local Similarity 99.8%; Pred. No. 8 6e-309;
Matches 427; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 15 CFAIIAIOQAQAVPNPAVDEVRSNDGONELPIDVQSATQASSTDTANPLDEHEPE 74
DB 15 CFAIIAIOQAQAVPNPAVDEVRSNDGONELPIDVQSATQASSTDTANPLDEHEPE 74
OY 75 LYTTALENTKMLINCSALNODIMRLACYDTLVHGETPAVTKTKRSIRLDDETWTQIKGR 134
DB 75 LYTTALENTKMLINCSALNODIMRLACYDTLVHGETPAVTKTKRSIRLDDETWTQIKGR 134
OY 135 QVYQETTDPIFLMGNEKGMILTKKAKOLEYAKOFTPLSLSDLDNRNTPLMSSRPNNP 194
DB 135 QVYQETTDPIFLMGNEKGMILTKKAKOLEYAKOFTPLSLSDLDNRNTPLMSSRPNNP 194

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QY 195 MYVLPFMHGKPRSPNTPSHEAKOFTPNDFRAPBLKFOYSVKAAEDLMGTDSDLWFG 254
DB 195 MYVLPFMHGKPRSPNTPSHEAKOFTPNDFRAPBLKFOYSVKAAEDLMGTDSDLWFG 254
QY 255 YTOQSHMOJFNGKNSRPFVHDYQPEIFLTQPYSDLPMDGKVRMIGMGAHHSNESAK 314
DB 255 YTOQSHMOJFNGKNSRPFVHDYQPEIFLTQPYSDLPMDGKVRMIGMGAHHSNESAK 314
QY 315 LSRSNRRAYLTMAGMEKNLTVMPRIWGRIFKEGSGSQPDNDPILDYGYGQVRFYQLQE 374
DB 315 LSRSNRRAYLTMAGMEKNLTVMPRIWGRIFKEGSGSQPDNDPILDYGYGQVRFYQLQE 374
QY 375 NNSNIGTFRVNPGRSGKALQIDYVPLGKISGYFOITQGYQOSLIDVNHETSFGVGL 434
DB 375 NNSNIGTFRVNPGRSGKALQIDYVPLGKISGYFOITQGYQOSLIDVNHETSFGVGL 434
QY 435 MLNDMMGL 442
DB 435 MLNDMMGL 442

RESULT 3
AA017569
ID AA017569 standard; Protein; 289 AA.
XX
AC AA017569;
XX
DT 19-JUL-2002 (first entry)
XX
DE M catarrhalis MCA100712 protein seq ID NO: 18.
XX
KM Moraxella; vaccine; respiratory tract infection; antinflammatory;
XX auditory; antibacterial; otitis media; sinusitis; pneumonia.
XX
OS Moraxella catarrhalis.
XX
PN WO200218595-A2.
XX
PD 07-MAR-2002.
XX
PF 28-AUG-2001; 2001WO-CA01221.
XX
PR 28-AUG-2000; 2000US-228294P.
PR 28-AUG-2000; 2000US-228295P.
PR 29-AUG-2000; 2000US-228438P.
PR 29-AUG-2000; 2000US-228439P.
PR 29-AUG-2000; 2000US-228440P.
PR 29-AUG-2000; 2000US-228441P.
PR 29-AUG-2000; 2000US-228442P.
PR 29-AUG-2000; 2000US-228443P.
PR 29-AUG-2000; 2000US-228511P.
PR 29-AUG-2000; 2000US-228512P.
PR 29-AUG-2000; 2000US-228742P.
PR 01-SEP-2000; 2000US-229465P.
PR 01-SEP-2000; 2000US-229474P.
PR 01-SEP-2000; 2000US-229475P.
PR 01-SEP-2000; 2000US-229478P.
PR 05-SEP-2000; 2000US-229740P.
PR 05-SEP-2000; 2000US-229803P.
PR 05-SEP-2000; 2000US-229804P.
PR 05-SEP-2000; 2000US-229805P.
PR 05-SEP-2000; 2000US-229806P.
PR 05-SEP-2000; 2000US-229809P.
PR 05-SEP-2000; 2000US-229811P.
PR 06-SEP-2000; 2000US-230214P.
PR 06-SEP-2000; 2000US-230250P.
PR 06-SEP-2000; 2000US-230252P.
XX
XX (AVERT ) AVENTIS PASTEUR LTD.
PA
XX
PI
XX
XX Loosmore S, Wang J, Bradley B, Ochs M, Yang Y;

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XX
DR WPI; 2002-401721/43.
DR N-PSDB; AAL46501.
XX
PT Moraxella polypeptide and polynucleotides useful as vaccine for
PT immunizing a host e.g. humans against disease e.g. otitis media,
PT pneumonia, caused by infection of the bacteria
XX
PS Claim 28; Fig 17; 277pp; English.
XX
XX The present invention provides the protein and coding sequences of
CC proteins from Moraxella catarrhalis. These can be used to produce
CC vaccines which protect against M. catarrhalis infection, which can cause
CC otitis media, respiratory infection, sinusitis, and pneumonia. The
CC present sequence is a protein of the invention.
XX
SQ Sequence 289 AA;
XX
Query Match 65.4%; Score 289; DB 23; Length 289;
Best Local Similarity 100.0%; Pred. No. 4.7e-272;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 154 MLTKKAKOLEYAKOFTPLSFDDLRNTPMSSRPHNPVLPFIMHGKPNRSPNTP 213
DB 1 MLTKKAKOLEYAKOFTPLSFDDLRNTPMSSRPHNPVLPFIMHGKPNRSPNTP 60
QY 214 SHEAKOFTPNDFRAPBLKFOYSVKAAEDLMGTDSDLWEGYTOQSHMOJFNGKNSRPF 273
DB 61 SHEAKOFTPNDFRAPBLKFOYSVKAAEDLMGTDSDLWEGYTOQSHMOJFNGKNSRPF 120
QY 274 VHDYQPEIFLTQPYSDLPMDGKVRMIGMGAHHSNESAKLSRSNRRAYLTMAGMEKNL 333
DB 121 VHDYQPEIFLTQPYSDLPMDGKVRMIGMGAHHSNESAKLSRSNRRAYLTMAGMEKNL 180
QY 334 TVMPRIWGRIFKEGSGSQPDNDPILDYGYGQVRFYQLQENKSNISGTVRNPGRSGKA 393
DB 181 TVMPRIWGRIFKEGSGSQPDNDPILDYGYGQVRFYQLQENKSNISGTVRNPGRSGKA 240
QY 394 LQLDYVYPLGKISGYFOITQGYQOSLIDVNHETSFGVGLMLNDMMGL 442
DB 241 LQLDYVYPLGKISGYFOITQGYQOSLIDVNHETSFGVGLMLNDMMGL 289

RESULT 4
AA085269
ID AA085269 standard; Protein; 442 AA.
XX
AC AA085269;
XX
DT 29-JUN-2000 (first entry)
XX
DE BASB034 amino acid sequence #2.
XX
KM Moraxella catarrhalis infection; BASB034; diagnosis; staging;
KM vaccine; bacteriostatic; treatment; prevention; otitis media; pneumonia;
KM sinusitis; nosocomial infection; invasive disease; chronic otitis media;
KM hearing loss; antibacterial drug.
XX
XX Moraxella catarrhalis.
OS
PN WO200015802-A1.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-EP06781.
XX
PR 14-SEP-1998; 98GB-0020002.
XX
XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX
PI
XX
XX Ruelle J;
XX
XX WPI; 2000-271440/23.
DR

```

XX	N-PSDB; AAA10701.
PT	Novel BASB034 polynucleotides and polypeptides from Moraxella
XX	catarrhalis used to prepare vaccines against bacterial infections -
XX	Claim 3; Page 67; 106pp; English.
CC	This sequence represents a Moraxella catarrhalis BASB034 polypeptide from
CC	strain Mc2908. The invention relates to BASB034 polypeptides from
CC	M. catarrhalis strains Mc2931, Mc2908, Mc2913 and Mc2969. The BASB034
CC	polynucleotides and polypeptides can be employed as research reagents and
CC	material for the discovery of treatments and diagnostics for diseases,
CC	particularly human diseases. They are particularly used to diagnose and
CC	treat M. catarrhalis infections. They can be used for diagnosis of
CC	disease, staging of disease, or determining response of an infectious
CC	organism to drugs. The polynucleotides may be used as a source for
CC	hybridization probes, and for screening of genetic mutations, serotype,
CC	sequencing or strain identification. Identification of mutations in BASB034
CC	organisms, and as components of arrays which are useful for diagnostic
CC	and prognostic purposes. The polypeptides can be used to produce
CC	antibodies. The polypeptides can also be used in vaccine formulations,
CC	and to identify agonists and antagonists. The polypeptides, antibodies,
CC	agonists and antagonists (which are bacteriostatic) are used for the
CC	treatment and prevention of diseases such as otitis media in infants and
CC	children, pneumonia in elderlies, sinusitis, nosocomial infections and
CC	invasive diseases, and chronic otitis media with hearing loss. The
CC	polypeptides, agonists and antagonists are also used for screening of
CC	antibacterial drugs. The BASB034 products of the invention can be used
CC	screen for new antibacterial compounds that may target resistant
CC	bacteria.
XX	
SQ	Sequence 442 AA;
Query Match	50.7%; Score 224; DB 21; Length 442;
Best Local Similarity	100.0%; Pred. No. 8.6e-209;
Matches 224; Conservative	0; Mismatches 0; Indels 0; Gaps 0
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Db	219 QTPREFAPRLKPFVSVKYKAEDLMGDSLMLGYTQSIMQLFGNKSRRFRHNDQ 278
QY	279 PEIPLTGVPVSDLPMDGVKRMIGMAVNHSNGESAKLSRWNRATYLDAEMENKLTVMPR 338
Db	279 PEIPLTGVPVSDLPMDGVKRMIGMAVNHSNGESAKLSRWNRATYLDAEMENKLTVMPR 338
QY	339 IWGRIFKSGSGSQRPDNDPILDYTGVDYRFLYLENKSNISGTAVYNPRSGKALQIDLY 398
Db	339 IWGRIFKSGSGSQRPDNDPILDYTGVDYRFLYLENKSNISGTAVYNPRSGKALQIDLY 398
QY	399 VYPLKGISGGYFOIRFGQGSLIDVNHHEATSPGVGLMLDNMGL 442
Db	399 VYPLKGISGGYFOIRFGQGSLIDVNHHEATSPGVGLMLDNMGL 442
RESULT 5	
ID	AA852270
AC	AA852270 standard; Protein; 442 AA.
XX	
XX	AA852270;
DT	29-JUN-2000 (first entry)
DE	BASB034 amino acid sequence #3.
XX	
KW	Moraxella catarrhalis infection; BASB034; diagnosis; staging;
KW	vaccine; bacteriostatic; treatment; prevention; otitis media; pneumonia;
KW	sinusitis; nosocomial infection; invasive disease; chronic otitis media;
XX	hearing loss; antibacterial drug.
CS	
XX	Moraxella catarrhalis.
XN	
XX	MO200015802-A1.

PD	23-MAR-2000.
XX	14-SEP-1999; 99WO-EP06781.
XX	14-SEP-1998; 98GB-0020002.
PR	(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA	Ruelle J:
XX	WPI: 2000-271440/23.
DR	N-PSDB: AAA10702.
PT	Novel BASB034 polynucleotides and polypeptides from Moraxella
XX	catarrihalis used to prepare vaccines against bacterial infections
PS	Claim 3; Page 68; 106pp: English.
XX	This sequence represents a Moraxella catarrihalis BASB034 polypeptide from
CC	strain Mc2913. The invention relates to BASB034 polypeptides from
CC	M. catarrihalis strains Mc2931, Mc2908, Mc2913 and Mc2969. The BASB034
CC	polynucleotides and polypeptides may be employed as research reagents and
CC	material for the discovery of treatments and diagnostics for diseases, and
CC	particularly human diseases. They are particularly used to diagnose and
CC	treat M. catarrihalis infections. They can be used for diagnosis of
CC	disease, staging of disease, or determining response of an infectious
CC	organism to drugs. The polynucleotides may be used as a source for
CC	hybridization probes, and for screening of genetic mutations, serotype,
CC	orphanism or strain identification. Identification of mutations in BASB034
CC	sequences, and as components of arrays which are useful for diagnostic
CC	and prognostic purposes. The polypeptides can be used to produce
CC	antibodies. The polypeptides can also be used in vaccine formulations,
CC	and to identify agonists and antagonists. The polypeptides, antibodies,
CC	agonists and antagonists (which are bacteriostatic) are used for the
CC	treatment and prevention of diseases such as otitis media in infants and
CC	children, pneumonia in elderly, sinusitis, nosocomial infections and
CC	invasive diseases, and chronic otitis media with hearing loss. The
CC	polypeptides, agonists and antagonists are also used for screening of
CC	antibacterial drugs. The BASB034 products of the invention can be used
CC	screen for new antibacterial compounds that may target resistant
CC	bacteria.
SQ	Sequence 442 AA;
YY	Query Match 50.7%; Score 224; DB 21; Length 442;
YY	Best Local Similarity 100.0%; Pred. No. 8.6e-209; Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	219 QFTPEFAPRLKPFVSVYKAABEDLMTGSDSLMEGYTOOSHQLTFNGKNSRPFVRNDXO 278
Db	219 QFTPEFAPRLKPFVSVYKAABEDLMTGSDSLMEGYTOOSHQLTFNGKNSRPFVRNDXO 278
OY	279 PEIPLTOPYUSDLPMDGKYRMITGMCAVHNHSGESAKLSRSNRRATYLMAGEMKNLTVMFR 338
Db	279 PEIPLTOPYUSDLPMDGKYRMITGMCAVHNHSGESAKLSRSNRRATYLMAGEMKNLTVMFR 338
OY	339 IMGRIFKESSGSQPDPDNPILDYIGTGIDVKFLYOLENKSNISGTVAUNRSKGATOLDY 398
Db	339 IMGRIFKESSGSQPDPDNPILDYIGTGIDVKFLYOLENKSNISGTVAUNRSKGATOLDY 398
OY	399 VYPLGKISGVYFOIFOGYGOSLDIVNHHEATSGVGCLMLDMWGL 442
Db	399 VYPLGKISGVYFOIFOGYGOSLDIVNHHEATSGVGCLMLDMWGL 442
RESULT 6	
AC	ABG18034 standard; Protein: 255 AA.
XX	ABG18034;
DT	18-FEB-2002 (first entry)

DE		Novel human diagnostic protein #18025.
XX		
KW		Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW		food supplement; medical imaging; diagnostic; genetic disorder.
XX		
OS		Homo sapiens.
XX		
PN		WO200175067-A2.
PD		
PD		11-OCT-2001.
PE		
PF		30-MAR-2001; 2001WO-US08631.
XX		
PR		31-MAR-2000; 2000US-0540217.
PR		23-AUG-2000; 2000US-0649167.
XX		
PA		(HXSE-) HXSEQ INC.
XX		
PI		Drimac RT, Liu C, Tang YT;
XX		
DR		WPI: 2001-639362/73.
DR		N-PSDB; AAS82221.
XX		
PT		New isolated polynucleotide and encoded polypeptides, useful in
PT		diagnostics, forensics, gene mapping, identification of mutations
PT		responsible for genetic disorders or other traits and to assess
PT		biodiversity -
PS		
PS		Claim 20; SEQ ID NO 48393; 103bp; English.
XX		
CC		The invention relates to isolated polynucleotide (I) and
CC		polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC		polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC		and gene mapping, and in recombinant production of (II). The
CC		polynucleotides are also used in diagnostics as expressed sequence tags
CC		for identifying expressed genes. (I) is useful in gene therapy techniques
CC		to restore normal activity of (II) or to treat disease states involving
CC		(II). (II) is useful for generating antibodies against it, detecting or
CC		quantitating a polypeptide in tissue, as molecular weight markers and as
CC		a food supplement. (II) and its binding partners are useful in medical
CC		imaging of sites expressing (II). (I) and (II) are useful for treating
CC		disorders involving aberrant protein expression or biological activity.
CC		The polypeptide and polynucleotide sequences have applications in
CC		diagnostics, forensics, gene mapping, identification of mutations
CC		responsible for genetic disorders or other traits to assess biodiversity
CC		and to produce other types of data and products dependent on DNA and
CC		amino acid sequences. ABG00010-ABG030377 represent novel human
CC		diagnostic amino acid sequences of the invention.
CC		Note: The sequence data for this patent did not appear in the printed
CC		specification, but was obtained in electronic format directly from WIPO
CC		at ftp.wipo.int/pub/published_pct_sequences.
XX		
SQ		Sequence 255 AA:
OY		
DB		
Query Match	2.08;	Score 9; DB 22; Length 255;
Best Local Similarity	100.0%;	Pred. No. 2.9;
Matches 9; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
204 PEIFLOPY 212		
279 PEIFLOPY 287		
RESULT 7		
AAY7S156		
ID	AAY7S156 standard; Protein; 370 AA.	
XX		
AC	AAY7S156;	
XX		
DT	21-MAR-2000 (first entry)	
DE	Neisseria gonorrhoeae ORF 582 protein sequence SEQ ID NO:1786.	
XX		

KM		Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW		antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KV		antibacterial; gene therapy.
XX		
OS		Neisseria gonorrhoeae.
XX		
FN		W09957280-A2.
XX		
PD		11-NOV-1999.
XX		
PF		.30-APR-1999; 99WO-US09346.
XX		
PR		01-MAY-1998; 98US-0083758.
XX		
PR		31-JUL-1998; 98US-0094869.
XX		
PR		02-SEP-1998; 98US-0098994.
XX		
PR		02-SEP-1998; 98US-0099062.
XX		
PR		09-OCT-1998; 98US-0103749.
XX		
PR		09-OCT-1998; 98US-0103794.
XX		
PR		09-OCT-1998; 98US-0103796.
XX		
PR		25-FEB-1999; 99US-0121528.
XX		
PA		(CHIR) CHIRON CORP.
XX		
PA		(GENO-) INST GENOMIC RES.
XX		
PI		Fraser C, Galeotti C, Grandi G, Hickey E, Massignani V, Mora M;
XX		
PI		Petersen J, Piza M, Rappucci R, Ratti G, Scalato E, Scarselli M;
XX		
PI		Tetrellin H, Venter JC;
XX		
XX		
DR		WPI: 2000-062150/05.
XX		
DR		N-P8DB; AAZ53818.
XX		
PT		Novel Neisserial polypeptides predicted to be useful antigens for
XX		
PT		vaccines and diagnostics -
XX		
PS		Claim 2; Page 903; 145pp; English.
XX		
CC		AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
XX		
CC		represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
XX		and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
CC		PCR primers used in the exemplification of the present invention. The
XX		
CC		polypeptides, the polynucleotides, antibodies and compositions of
XX		
CC		the invention can be used as vaccines, as diagnostic reagents, and as
XX		
CC		immunogenic compositions. The polypeptides can be used in the
XX		
CC		manufacture of medicaments for treating or preventing infection due to
XX		
CC		Neisserial bacteria (e.g. meningitis and septicemia), to detect the
XX		
CC		presence of Neisseria bacteria, or to raise antibodies. They may also
XX		
CC		be used to screen for agonists or antagonists, which may themselves
XX		
CC		have use as antibacterial agents. The polynucleotides of the invention
XX		
CC		may also be used in gene therapy protocols.
XX		
SQ		Sequence 370 AA;
XX		
Query Match		2.0%; Score 9; DB 21; Length 370;
Best Local Similarity		100.0%; Pred. No. 4;
Matches 9; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
Oy		279 PEIFLTOPY 287
Db		209 PEIFLTOPY 217
XX		
RESULT 8		
AA75157		
ID		AA75157 standard; Protein; 370 AA.
XX		
AC		AA75157;
XX		
DT		21-MAR-2000 (first entry)
XX		
DE		Neisseria meningitidis ORF 582 protein sequence SEQ ID NO:1788.
XX		
KM		Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW		antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KV		antibacterial; gene therapy.

```

KW antibacterial; gene therapy.
XX
OS Neisseria meningitidis.
XX
PN W09957280-A2.
XX
PD 11-NOV-1999.
XX
PE 30-APR-1999; 99WO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
XX PR 31-JUL-1998; 98US-0094869.
XX PR 02-SEP-1998; 98US-0098994.
XX PR 02-SEP-1998; 98US-0099062.
XX PR 09-OCT-1998; 98US-0103749.
XX PR 09-OCT-1998; 98US-0103794.
XX PR 09-OCT-1998; 98US-0103796.
XX PR 25-FEB-1999; 99US-0121528.
XX
PA (CHIR ) CHIRON CORP.
XX (GENO-) INST GENOMIC RES.
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizsa M, Rappunlt R, Ratel G, Scalato E, Scarselli M;
PI Tettelein H, Venter JC;
XX
DR WPJ; 2000-062150/05.
DR N-PSDB; AAZ53919.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics -
XX
PS Claim 2; Page 904; 1453pp; English.
XX
AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ54773 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC Neisserial bacteria (e.g. meningitis and septicaemia) to detect the
CC presence of Neisseria bacteria, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
XX
SQ Sequence 370 AA;
Query Match 2.0%; Score 9; DB 21; Length 370;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 279 PEIPLTGPV 287
Db 209 PEIPLTGPV 217
|||||
|||

RESULT 9
AAID ID AAY75158 standard; Protein: 370 AA.
AC AAY75158;
XX
XX AAY75158;
DT 21-MAR-2000 (first entry)
XX
XX Neisseria meningitidis ORF 582 protein sequence SEQ ID NO:1790.
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
antibacterial; gene therapy.
XX
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OS	Neisseria meningitidis.
PN	W09557280-AAZ.
PD	11-NOV-1999.
PF	30-APR-1999; 99WO-US09346.
PR	01-MAY-1998; 98US-0083758.
PR	31-JUL-1998; 98US-0094869.
PR	02-SEP-1998; 98US-0098994.
PR	02-SEP-1998; 98US-0099062.
PR	09-OCT-1998; 98US-0103749.
PR	09-OCT-1998; 98US-0103794.
PR	09-OCT-1998; 98US-0103796.
PR	25-FEB-1999; 99US-0121528.
PA	(CHIR) CHIRON CORP.
PA	(GENO-) INST GENOMIC RES.
PI	Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M,
PI	Petersen J, Pizzo M, Rappunli R, Ratti G, Scalato E, Scarselli M,
PI	Tetzelin H, Venter JC;
XX	WPI: 2000-062150/05.
DR	N-PSTB; AAZ53920.
XX	Novel Neisserial polypeptides predicted to be useful antigens for
PT	vaccines and diagnostics -
PS	Claim 2; Page 905; 1453pp; English.
CC	AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC	represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC	and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ54473 represent
CC	PCR primers used in the exemplification of the present invention. The
CC	polypeptides, the polynucleotides, antibodies and compositions of
CC	the invention can be used as vaccines, as diagnostic reagents, and as
CC	immunogenic compositions. The polypeptides can be used in the
CC	manufacture of medicaments for treating or preventing infection due to
CC	Neisserial bacteria (e.g. meningitis and septicaemia), to detect the
CC	presence of Neisseria bacteria, or to raise antibodies. They may also
CC	have been used to screen for agonists or antagonists, which may themselves
CC	have also been used in gene therapy protocols.
CC	
SQ	Sequence 370 AA;
Query Match	2.0%; Score 9; DB 21; Length 370;
Best Local Similarity	100.0%; Pred. No. 4;
Matches 9; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	279 PEFLTPGV 287
DB	.209 PEFLTPGV 217
RESULT 10	
ID	AAY70629
AA	AAY70629 standard; Protein; 374 AA.
AC	AAY70629;
DT	18-JUL-2000 (first entry)
DE	Neisseria meningitidis serogroup B strain H44/76 BASB033 protein.
XX	
KM	BASB033; diagnosis; prophylaxis; treatment; antibacterial; vaccine;
XX	Neisseria meningitidis infection.
OS	Neisseria meningitidis.
NN	W0200015801-A1.

XX 23-MAR-2000.
PD 09-SEP-1999; 99WO-EP06718.
XX 14-SEP-1998; 98GB-0020003.
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX Ruelle J;
XX WPI: 2000-271439/23.
DR N-PSDB; AAZ52134.
XX
PT Isolated BASB033 polypeptides and polynucleotides of Neisseria
PT meningitidis, useful for diagnosis, prophylaxis and treatment of N.
PT meningitidis infection -
PS Claim 4; Page 59; 93pp; English.
XX
CC The present sequence is a BASB033 protein from
CC Neisseria meningitidis serogroup B strain H44/76. The protein
CC shows homology to the Klebsiella pneumoniae outer membrane
CC phospholipase A. The present sequence is useful for diagnosis,
CC prophylaxis and treatment of N. meningitidis infection. It may also be
CC used for the discovery and development of antibacterial compounds and
CC in vaccine compositions.
XX
SQ Sequence 374 AA;
QY 279 PEIPLTOPV 287
Db 213 PEIPLTOPV 221
Query Match 2.0%; Score 9; DB 21; Length 374;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 279 PEIPLTOPV 287
Db 213 PEIPLTOPV 221
RESULT 11
AA70628
ID AA70628 standard; Protein: 375 AA.
XX
AC AA70628;
XX
DT 18-JUL-2000 (first entry)
XX
DE Neisseria meningitidis serogroup B strain ATCC13090 BASB033 protein.
XX
KW BASB033; diagnosis, prophylaxis; treatment; antibacterial; vaccine;
KW Neisseria meningitidis infection.
XX
OS Neisseria meningitidis.
XX
PN WO200015801-A1.
XX
PD 23-MAR-2000.
XX
PF 09-SEP-1999; 99WO-EP06718.
XX
PR 14-SEP-1998; 98GB-0020003.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PI Ruelle J;
XX
DR WPI: 2000-271439/23.
DR N-PSDB; AAZ52133.
PT Isolated BASB033 polypeptides and polynucleotides of Neisseria
PT meningitidis, useful for diagnosis, prophylaxis and treatment of N.
PT meningitidis infection -
XX

PS Claim 4; Page 58; 93pp; English.
XX
CC The present sequence is a BASB033 protein from
CC Neisseria meningitidis serogroup B strain ATCC13090. The protein
CC shows homology to the Klebsiella pneumoniae outer membrane
CC phospholipase A. The present sequence is useful for diagnosis,
CC prophylaxis and treatment of N. meningitidis infection. It may also be
CC used for the discovery and development of antibacterial compounds and
CC in vaccine compositions.
XX
SQ Sequence 375 AA;
QY 279 PEIPLTOPV 287
Db 214 PEIPLTOPV 222
Query Match 2.0%; Score 9; DB 21; Length 375;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 279 PEIPLTOPV 287
Db 214 PEIPLTOPV 222
RESULT 12
AAG1137
ID AAG1137 standard; Protein: 278 AA.
XX
AC AAG1137;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9741.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134376.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137328.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139889.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140655.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142390.
PR 09-JUL-1999; 99US-0142803.
PR 12-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
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PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.

PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147712.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149920.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.

PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 1.8%; Score 8; DB 21; Length 278;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 174 SLSFDLDR 181
| | | | |
Db 271 SLSFDLDR 278

RESULT 13
AA01136
ID AA01136 standard; Protein; 283 AA.

XX AC AA01136;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 9740.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP103405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 200DEP-0301439.

XX PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
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Best Local Similarity 100.0%; Pred. No. 30;

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AC AAG1135;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 9739.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
OS Arabidopsis thaliana.
PN
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PD
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PE 25-FEB-2000; 2000EP-0301439.
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Best Local Similarity 100.0%; Pred. No. 31;

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Qy 174 SLSPDLR 181
Db 292 SLSPDLR 299

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KW framework region; complementarity determining region; reshaping;
KW modelling; surface residue; modify.
XX
OS Mus sp.
XX
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XX
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PF 07-SEP-1993; 93EP-0307051.
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PR 09-SEP-1992; 92US-0942245.
XX
PA (PEDE/) PEDERSEN J T.
PA (IMMU-) IMMUNOGEN INC.
XX
PI Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
XX
DR WPI; 1994-120230/15.
XX
PT Method of resurfacing of rodent antibodies to produce humanised
PT antibody forms - for producing non-human antibodies with improved
PT therapeutic efficiency by presenting human surface on V-region
XX
PS Example 1; Page 14; 230pp; English.
XX
CC Modification of a rodent antibody or fragment by resurfacing in order
CC to produce a humanised rodent antibody can be determined by calculating
CC homology between murine and human antibody surfaces. In order to test
CC the resurfacing approach of the invention, three humanisation
CC experiments were set up. (1) traditional loop grafting; (2) resurfacing
CC approach using most similar chain; and (3) resurfacing approach using
CC human sequences with most similar surface residues. AAR52069-159 are the
CC surface residue patterns in mouse light chain antibody variable regions.
CC These "patches" were used in the third method, where rodent light and
CC heavy chains were matched and the most similar human sequence found
CC independently only over the surface residues indicated in AAR52030-67.
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SQ Sequence 16 AA;

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Db 4 PRSGKA 10

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:46 ; Search time 11 Seconds
(without alignments)
1182.267 Million cell updates/sec

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Searched: 262574 seqs, 29422922 residues

Word size : 0

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Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	7	1.6	347	4	US-09-097-889-14 Sequence 14, Appl
3	7	1.6	552	1	US-08-231-729B-6 Sequence 6, Appl
4	7	1.6	900	4	US-08-890-865A-4 Sequence 4, Appl
5	7	1.6	934	1	US-08-215-805A-80 Sequence 80, Appl
6	7	1.6	1026	2	US-08-542-003-6 Sequence 6, Appl
7	7	1.6	1026	4	US-08-322-760A-6 Sequence 6, Appl
8	7	1.6	1026	4	US-09-236-949-6 Sequence 6, Appl
9	6	1.4	10	3	US-08-974-775-30 Sequence 30, Appl
10	6	1.4	11	3	US-08-974-775-29 Sequence 29, Appl
11	6	1.4	12	3	US-08-974-775-28 Sequence 28, Appl
12	6	1.4	13	3	US-08-974-775-8 Sequence 8, Appl
13	6	1.4	13	3	US-08-974-775-27 Sequence 27, Appl
14	6	1.4	14	3	US-08-974-775-9 Sequence 9, Appl
15	6	1.4	14	3	US-08-974-775-10 Sequence 10, Appl
16	6	1.4	14	3	US-08-974-775-32 Sequence 32, Appl
17	6	1.4	15	3	US-08-974-775-5 Sequence 5, Appl
18	6	1.4	16	3	US-08-974-775-4 Sequence 4, Appl
19	6	1.4	20	1	US-08-430-273-1 Sequence 1, Appl
20	6	1.4	21	1	US-07-918-953-13 Sequence 13, Appl
21	6	1.4	21	1	US-07-918-953-15 Sequence 15, Appl
22	6	1.4	21	1	US-08-212-696-1 Sequence 1, Appl
23	6	1.4	21	1	US-08-158-245-1 Sequence 1, Appl
24	6	1.4	21	1	US-08-081-661-13 Sequence 13, Appl
25	6	1.4	21	1	US-08-081-661-15 Sequence 15, Appl
26	6	1.4	21	1	US-08-233-617-1 Sequence 1, Appl
27	6	1.4	21	1	US-08-160-376A-1 Sequence 1, Appl

28	6	1.4	21	1	US-08-304-070-1 Sequence 1, Appl
29	6	1.4	21	1	US-08-285-661-1 Sequence 1, Appl
30	6	1.4	21	1	US-08-301-838-1 Sequence 1, Appl
31	6	1.4	21	1	US-08-389-487-4 Sequence 4, Appl
32	6	1.4	21	1	US-08-389-487-12 Sequence 12, Appl
33	6	1.4	21	1	US-08-507-124-2 Sequence 2, Appl
34	6	1.4	21	1	US-08-507-124-3 Sequence 3, Appl
35	6	1.4	21	1	US-08-342-931-1 Sequence 1, Appl
36	6	1.4	21	1	US-08-400-256-1 Sequence 1, Appl
37	6	1.4	21	2	US-08-508-664-9 Sequence 9, Appl
38	6	1.4	21	2	US-08-353-476-85 Sequence 85, Appl
39	6	1.4	21	2	US-08-353-476-87 Sequence 87, Appl
40	6	1.4	21	2	US-08-484-219-1 Sequence 1, Appl
41	6	1.4	21	2	US-08-979-587-1 Sequence 1, Appl
42	6	1.4	21	2	US-08-992-676-1 Sequence 1, Appl
43	6	1.4	21	2	US-08-992-676-6 Sequence 6, Appl
44	6	1.4	21	2	US-09-134-836-1 Sequence 1, Appl
45	6	1.4	21	2	US-09-134-836-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-07-942-245-98
Sequence 98, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Brian C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sugrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 workstation
OPERATING SYSTEM: UNIX
SOFTWARE: in house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-98

Query Match 1.6%; Score 7; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 387 PRSGKGA 393
|||||||
Db 4 PRSGKGA 10

RESULT 2
US-09-097-889-14
Sequence 14, Application US/09097889
Patent No. 6218117
GENERAL INFORMATION:
APPLICANT: Herrstadt, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
TITLE OF INVENTION: AGENTS THAT QUANTITATIVELY ALTER DETECTABLE
TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,889
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.417
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-097-889-14

Query Match 1.6%; Score 7; DB 4; Length 347;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LTLSTLS 14
|||||||
DB 155 LTLSTLS 161

RESULT 3
US-08-231-729B-6
Sequence 6, Application US/08231729B
Patent No. 5618722
GENERAL INFORMATION:
APPLICANT: ZENNO, Shunei
APPLICANT: SHIRAIISHI, Shinji
APPLICANT: INOUE, Satoshi
APPLICANT: SAIGO, Kaoru
TITLE OF INVENTION: FIREFLY LUCIFERASE GENE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER
STREET: 700 Thirteenth Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,729B
FILING DATE: 20-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 119050/1993
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rose, Herbert C.
REGISTRATION NUMBER: 29846
REFERENCE/DOCKET NUMBER: 60130/NO. 5618722aka
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-6770
TELEFAX: 202-737-6776
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-231-729B-6

Query Match 1.6%; Score 7; DB 1; Length 552;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 LSFDDLR 181
|||||||
DB 184 LSFDDLR 190

RESULT 4
US-08-890-865A-4
Sequence 4, Application US/08890865A
Patent No. 6307019
GENERAL INFORMATION:
APPLICANT: Constantini, Franklin
APPLICANT: Zeng, Li
TITLE OF INVENTION: AXIN GENE AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,865A
FILING DATE: 10-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/54249
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-890-865A-4

Query Match 1.6%; Score 7; DB 4; Length 900;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 GKGISGY 409
|||||
DB 268 GKGISGY 274

RESULT 5

US-08-215-805A-80
; Sequence 80, Application US/08215805A
; Patent No. 5559008
; GENERAL INFORMATION:
; APPLICANT: Chang, Yung-Fu
; TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURILLA
; TITLE OF INVENTION: SUI5
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/215,805A
; FILING DATE: 22-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Timlan, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 934 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Pasteurella suis
; STRAIN: 5943
; IMMEDIATE SOURCE:
; LIBRARY: P. suis DNA in Bacteriophage lambda-dash
; CLONE: (Lambda)yfc33-37
US-08-215-805A-80

Query Match 1.6%; Score 7; DB 1; Length 934;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 VKAAEDL 244
|||||
DB 62 VKAAEDL 68

RESULT 6

US-08-542-003-6
; Sequence 6, Application US/08542003
; Patent No. 5864013
; GENERAL INFORMATION:
; APPLICANT: Goldberg, Edward B.
; TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF

; TITLE OF INVENTION: NANOMETER STRUCTURES AND USE THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennile and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/542,003
; FILING DATE: 13-OCT-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8471-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: 212-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1026 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacteriophage T4
; IMMEDIATE SOURCE:
; CLONE: p37 amino acid
US-08-542-003-6

Query Match 1.6%; Score 7; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 QTIKGP 134
|||||
DB 861 QTIKGP 867

RESULT 7

US-08-322-760A-6
; Sequence 6, Application US/08322760A
; Patent No. 5877279
; GENERAL INFORMATION:
; APPLICANT: Goldberg, Edward B.
; TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF
; TITLE OF INVENTION: NANOMETER STRUCTURES AND USE THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennile and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/322,760A
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8471-0003-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: 212-869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacteriophage T4
IMMEDIATE SOURCE:
CLONE: p37 amino acid
US-08-322-760A-6

Query Match 1.6%; Score 7; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 QTIKGP 134
|||||
DB 861 QTIKGP 867

RESULT 8
US-09-236-949-6
Sequence 6, Application US/09236949
Patent No. 6437112

GENERAL INFORMATION:

APPLICANT: Goldberg, Edward B.
TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,949
FILING DATE: 25-Jan-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/542,003
FILING DATE: 13-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8471-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: 212-869-8864
TELEX: 66441 PENNIE

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Bacteriophage T4
IMMEDIATE SOURCE:

CLONE: p37 amino acid
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-236-949-6

Query Match 1.6%; Score 7; DB 4; Length 1026;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 QTIKGP 134
|||||
DB 861 QTIKGP 867

RESULT 9
US-08-974-775-30
Sequence 30, Application US/08974775
Patent No. 6096706

GENERAL INFORMATION:

APPLICANT: Toback, F. Gary
APPLICANT: Walsh-Reitz, Margaret
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Clyfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-30

Query Match 1.4%; Score 6; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 424 NHEATS 429
|||||
DB 5 NHEATS 10

RESULT 10
US-08-974-775-29

Sequence 29, Application US/08974775
Patent No. 6096706

GENERAL INFORMATION:

APPLICANT: Toback, F. Gary
APPLICANT: Walsh-Reitz, Margaret
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES

TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-29

Query Match 1.4%; Score 6; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
|||||
DB 5 NHEATS 10

RESULT 11
US-08-974-775-28
Sequence 28, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.

REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-28

Query Match 1.4%; Score 6; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
|||||
DB 5 NHEATS 10

RESULT 12
US-08-974-775-8
Sequence 8, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-8

Query Match 1.4%; Score 6; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
|||||
DB 8 NHEATS 13

RESULT 13
US-08-974-775-27
Sequence 27, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4299
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-27

Query Match 1.4%; Score 6; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
|||||
Db 5 NHEATS 10

RESULT 14
US-08-974-775-9
Sequence 9, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4299
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-9

Query Match 1.4%; Score 6; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
|||||
Db 8 NHEATS 13

RESULT 15
US-08-974-775-10
Sequence 10, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-974-775-10

Query Match 1.4%; Score 6; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 424 NHEATS 429
|||||
DB 8 NHEATS 13

Search completed: November 12, 2002, 11:49:11
Job time : 14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:45 ; Search time 13.75 Seconds
(without alignments)
3090.285 Million cell updates/sec

Title: US-09-787-083-2

Perfect score: 442

Sequence: 1 MKVSLSTLTLSLSCFALLA.....YNHEATSPGVGLMNDNMGL 442

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	9	2.0	382	2	E81195	phospholipase A1, probable phospholip outer membrane phospholipase A1
2	9	2.0	409	2	H81831	probable phospholip outer membrane phospholipase A1
3	8	1.8	286	2	B36971	RAV-like protein - L-shaped tail fibre
4	8	1.8	299	2	T47989	hypothetical prote
5	8	1.8	1396	2	S36851	hypothetical prote
6	7	1.6	68	2	B97871	probable membrane phospholipase A1
7	7	1.6	100	2	S61050	hypothetical prote
8	7	1.6	112	2	C97787	hypothetical prote
9	7	1.6	122	2	E75377	hypothetical prote
10	7	1.6	158	2	E86498	hypothetical prote
11	7	1.6	158	2	E72124	pts iia protein - integrase xerf fam
12	7	1.6	164	2	E97061	hypothetical prote
13	7	1.6	183	2	A12419	hypothetical prote
14	7	1.6	185	2	H90463	tubulin alpha-1 ch
15	7	1.6	197	2	A54506	hypothetical prote
16	7	1.6	219	2	T19438	tubulin alpha ch
17	7	1.6	233	2	AD3344	hypothetical prote
18	7	1.6	240	2	AD1544	tubulin alpha ch
19	7	1.6	264	2	A44959	coat protein - pot
20	7	1.6	267	2	A60366	coat protein - pot
21	7	1.6	267	2	S14001	genome polyprotein capsid protein - p
22	7	1.6	267	2	S26630	coat protein - pot
23	7	1.6	267	2	JC1527	coat protein - pot
24	7	1.6	267	2	S13239	tail fiber protein
25	7	1.6	267	2	E84092	phage-related prot
26	7	1.6	270	2	S73734	abc transport ATP-
27	7	1.6	273	2	C72328	transaminase B hom
28	7	1.6	287	2	A72421	oligopeptide ABC t
29	7	1.6	288	2	T36237	probable phosphot

30	7	1.6	306	2	T27985	hypothetical prote
31	7	1.6	307	2	B87659	hydrolase, probabl
32	7	1.6	310	2	T02200	probable RAV-like
33	7	1.6	313	2	JT0960	polyprotein - pota
34	7	1.6	321	2	H82240	conserved hypothet
35	7	1.6	324	2	T23876	hypothetical prote
36	7	1.6	326	2	A43939	proteinase inhibit
37	7	1.6	338	2	F69437	hypothetical prote
38	7	1.6	341	2	T47653	pectate lyase-like
39	7	1.6	342	2	G64411	hypothetical prote
40	7	1.6	342	2	C64394	hypothetical prote
41	7	1.6	343	2	AG2465	hypothetical prote
42	7	1.6	347	1	DNHUN2	NADH2 dehydrogenas
43	7	1.6	347	2	T11051	NADH2 dehydrogenas
44	7	1.6	347	2	B59153	NADH2 dehydrogenas
45	7	1.6	349	2	T43920	Yfuc protein [impo

ALIGNMENTS

RESULT 1
E81195
phospholipase A1, probable NMB0464 [imported] - Neisseria meningitidis (strain MC58 s
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: E81195
R:Retelkin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, R.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Douberly, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: AB1000; MUID:20175755; PMID:10710307
A:Accession: E81195
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-382 <RET>
A:Cross-references: GB:AE002403; GB:AE002098; NID:g7225688; PIDN:AAFA0901.1; PID:g722
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0464

Query Match 2.0%; Score 9; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 PEFLTPQPV 287
DB 221 PEFLTPQPV 229

RESULT 2

H81831
probable phospholipase NMA2021 [imported] - Neisseria meningitidis (strain Z2491 serog

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

R:Parhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo

; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Kungall, K.; Quail, M.A.; Rajandre

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491

A:Reference number: AB1775; MUID:20222596; PMID:10761919

A:Accession: H81831

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-409 <PAR>

A:Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85240.1; PID:g738

A:Experimental source: serogroup A, strain Z2491

C:Genetics:
A:Gene: NMA2021

Query Match 2.0%; Score 9; DB 2; Length 409;

Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 279 PEIFLTPV 287
|||||
DB 248 PEIFLTPV 256

RESULT 3
B36971
outer membrane phospholipase A (EC 3.1.1.-) precursor - Klebsiella pneumoniae
C:Species: Klebsiella pneumoniae
C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 18-Jun-1999
C:Accession: B36971; S40129
R:Brok, R.G.P.M.; Brinkman, E.; van Bontel, R.; Bekkers, A.C.A.P.A.; Verheij, H.M.; Tomm
J. Bacteriol. 176, 861-870, 1994
A:Title: Molecular characterization of enterobacterial plid genes encoding outer membran
A:Reference number: A36971; MUID:94131966; PMID:8300539
A:Accession: B36971
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-286 <BRO>
A:Cross-references: EMBL:X76901; NID:g436880; PIDN:CAA54223.1; PID:g436881
A:Note: authors translated the codon AAG for residue 112 as Arg
C:Genetics:
A:Gene: plid
C:Superfamily: bacterial phospholipase A1
C:Keywords: carboxylic ester hydrolase

Query Match 1.8%; Score 8; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 GVGMLND 438
|||||
DB 277 GVGMLND 284

RESULT 4
T47989
RAV-like protein - Arabidopsis thaliana
N:Alternate names: protein F21F14.140
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47989
R:Chastine, N.; Robert, C.; Brotlier, P.; Winkler, P.; Catolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, February 2000
A:Reference number: 224481
A:Accession: T47989
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-299 <CHO>
A:Cross-references: EMBL:AL138642
A:Experimental source: cultivar Columbia; BAC clone F21F14
C:Genetics:
A:Map position: 3
A:Note: F21F14.140

Query Match 1.8%; Score 8; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 SLSPDLR 181
|||||
DB 292 SLSPDLR 299

RESULT 5
S36851
L-shaped tail fiber protein - phage T5
N:Alternate names: ltf protein
C:Species: phage T5
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000

C:Accession: S65934; S01984; S36851
R:Kallim, A.V.; Kulshin, V.E.; Shiyapnikov, M.G.; Ksenzenko, V.N.; Kryukov, V.M.
FEBS Lett. 366, 46-48, 1995
A:Title: The nucleotide sequence of the bacteriophage T5 ltf gene.
A:Reference number: S65934; MUID:95309401; PMID:7789514
A:Accession: S65934

A:Molecule type: DNA
A:Residues: 1-1396 <KAL>
A:Cross-references: EMBL:X69460; NID:g15415; PIDN:CAA49220.1; PID:g15416
R:Kallim, A.V.; Kryukov, V.M.; Bayev, A.A.
Nucleic Acids Res. 16, 6230, 1988
A:Title: The nucleotide sequence of bacteriophage T5 DNA at the region between early
A:Reference number: S01982; MUID:88289370; PMID:3267228
A:Accession: S01984
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 934-985, A', 987-1396 <KA2>
A:Cross-references: EMBL:X07539
C:Genetics:
A:Gene: ltf
C:Keywords: late protein; tail fiber

Query Match 1.8%; Score 8; DB 2; Length 1396;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QSATOSAS 61
|||||
DB 87 QSATOSAS 94

RESULT 6
B97871
hypothetical protein RC1370 [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C:Accession: B97871
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: B97871
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-68 <KUR>
A:Cross-references: GB:AE006914; PIDN:AL03908.1; PID:g15620515; GSPDB:GN00173
C:Genetics:
A:Gene: RC1370

Query Match 1.6%; Score 7; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 TALENKT 84
|||||
DB 45 TALENKT 51

RESULT 7
S61050
probable membrane protein YDL163w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D1505
C:Species: Saccharomyces cerevisiae
C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 19-Apr-2002
C:Accession: S61050; S67715
R:Pohl, T.M.
submitted to the EMBL Data Library, November 1995
A:Reference number: S61050
A:Accession: S61050
A:Molecule type: DNA
A:Residues: 1-100 <POH>
A:Cross-references: EMBL:Z67750; NID:g1061256; PID:g1061276
R:Pohl, T.M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67708
A:Accession: S67715
A:Molecule type: DNA
A:Residues: 1-100 <POW>
A:Cross-references: EMBL:Z74212; NID:g1431258; PID:g1431260; MIPS:YDL163W
A:Experimental source: strain S288C
C:Genetics:
A:Cross-references: SGD:S0002322
A:Map position: 4L
C:Superfamily: Saccharomyces probable membrane protein YDL163W
C:Keywords: transmembrane protein
F:3.19/Domain: transmembrane #status predicted <TMM>

Query Match 1.6%: Score 7; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LSTLTL 14
|||||
Db 26 LSTLTL 32

RESULT 8

hypothetical protein RC0699 [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii

C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C:Accession: C97787
R:Ogata, H.; Audic, S.; Renseto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: C97787
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-112 <KUR>
A:Cross-references: GB:AE006914; PIDN:AA103237.1; PID:g15619790; GSPDB:GN00173
C:Genetics:
A:Gene: RC0699

Query Match 1.6%: Score 7; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 NDLAGDN 47
|||||
Db 85 NDLAGDN 91

RESULT 9

E75377
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: E75377
R:White, O.; Eissen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; M Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75377
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-122 <WHI>
A:Cross-references: GB:AE002002; GB:AE000513; NID:g6459345; PIDN:AA11150.1; PID:g6459345
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1580
A:Map position: 1

Query Match 1.6%: Score 7; DB 2; Length 122;

Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 70 EHEPELY 76
|||||
Db 115 EHEPELY 121

RESULT 10

E86498
pts. IIA Protein [imported] - Chlamydia pneumoniae (strain J138)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: E86498
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: E86498
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <STO>
A:Cross-references: GB:BA000008; NID:g8978434; PIDN:BAA98271.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: ptsN_1
C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannito

Query Match 1.6%: Score 7; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LSTLTL 11
|||||
Db 126 LSTLTL 132

RESULT 11

E72124
pts. IIA protein - Chlamydia pneumoniae (strain CML029)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C:Accession: E72124
R:Kaimin, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: E72124
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <ARN>
A:Cross-references: GB:AE001591; GB:AE001363; NID:g4376311; PIDN:AMD18213.1; PID:g437
A:Experimental source: strain CML029
C:Genetics:
A:Gene: ptsN_1
C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannito

F:28-156/Domain: phosphotransferase system mannitol-specific enzyme II factor III hom

Query Match 1.6%: Score 7; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LSTLTL 11
|||||
Db 126 LSTLTL 132

RESULT 12

E97061
integrase xerD family protein (similarity only with C-terminal part) [imported] - Clo
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: E97061

R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum* ATCC824
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: E97061
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-164 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK79280.1; PID:g15024240; GSPDB:GN00168
 A:Experimental source: *Clostridium acetobutylicum* ATCC824
 C:Genetics:
 A:Gene: CAC1310

Query Match 1.6%; Score 7; DB 2; Length 164;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 372 QLENKSN 378
 |||||||
 DB 49 QLENKSN 55

RESULT 13
 A12419
 Hypothetical protein alr4913 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: A12419
 R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: A12419
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-183 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BAW76612.1; PID:g17134051; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr4913

Query Match 1.6%; Score 7; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EVRSEND 42
 |||||||
 DB 104 EVRSEND 110

RESULT 14
 H90463
 Hypothetical protein SSO2858 [imported] - *Sulfolobus solfataricus*
 C:Species: *Sulfolobus solfataricus*
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
 C:Accession: H90463
 R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.
 submitted to GenBank, April 2001
 A:Description: *Sulfolobus solfataricus* complete genome.
 A:Reference number: A99139
 A:Accession: H90463
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-185 <KUR>
 A:Cross-references: GB:AE006641; NID:g13816218; PIDN:AAK42967.1; GSPDB:GN00155
 C:Genetics:
 A:Gene: SSO2858

Query Match 1.6%; Score 7; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 LTRSLIS 14
 |||||||
 DB 122 LTRSLIS 128

RESULT 15
 A54506
 tubulin alpha-1 chain - *Plasmodium yoelii* (fragment)
 C:Species: *Plasmodium yoelii*
 C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 13-Aug-1999
 C:Accession: A54506
 R:Akella, R.; Arasu, P.; Valdiva, A.B.
 Mol. Biochem. Parasitol. 30, 165-174, 1988
 A:Title: Molecular clones of alpha-tubulin genes of *Plasmodium yoelii* reveal an unusual
 A:Reference number: A54506; MUID:89014607; PMID:2459618
 A:Accession: A54506
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-197 <AKE>
 A:Cross-references: GB:M29816; NID:g160729; PIDN:AAA29779.1; PID:g160730
 C:Superfamily: tubulin

Query Match 1.6%; Score 7; DB 2; Length 197;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 IKTKRSI 120
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 DB 82 IKTKRSI 88

Search completed: November 12, 2002, 11:46:28
 Job time : 15.75 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:45:00 ; Search time 5.75 Seconds
(without alignments)
1108.344 Million cell updates/sec

Title: US-09-787-083-2

Perfect score: 442

Sequence: 1 MKVSLSTLSTLSCFALLA.....YHNEATSPCVGLMDNMGL 442

Scoring table:

GAPOP 60.0 , Gapect 60.0

Searched: 92612 seqs, 14418503 residues

Word size : 0

Total number of hits satisfying chosen parameters: 92612

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	1.6	75	10	US-09-764-869-1013
2	7	1.6	158	10	US-09-789-919-42
3	7	1.6	347	10	US-09-098-079-14
4	7	1.6	511	10	US-09-773-882-2
5	7	1.6	511	10	US-09-773-882-11
6	7	1.6	513	10	US-09-815-242-11029
7	7	1.6	783	10	US-09-825-144-2
8	7	1.6	829	10	US-09-825-144-4
9	6	1.4	15	10	US-09-947-770-20
10	6	1.4	17	10	US-09-732-561-23
11	6	1.4	21	9	US-09-947-563-1
12	6	1.4	21	9	US-09-947-563-7
13	6	1.4	21	10	US-09-853-844-1
14	6	1.4	21	10	US-09-815-229-1
15	6	1.4	22	12	US-10-066-151-102
16	6	1.4	26	10	US-09-864-761-43426
17	6	1.4	28	12	US-10-014-269-9
18	6	1.4	30	10	US-09-815-229-16
19	6	1.4	33	10	US-09-030-619-175

20	6	1.4	39	10	US-09-205-658-116	Sequence 116, App
21	6	1.4	39	12	US-10-042-417-18	Sequence 18, Appl
22	6	1.4	46	10	US-09-203-658-132	Sequence 132, App
23	6	1.4	46	10	US-09-205-658-133	Sequence 133, App
24	6	1.4	46	10	US-09-205-658-136	Sequence 136, App
25	6	1.4	48	10	US-09-891-171-10	Sequence 10, Appl
26	6	1.4	50	10	US-09-853-844-4	Sequence 4, Appl1
27	6	1.4	50	10	US-09-864-761-41965	Sequence 41965, A
28	6	1.4	51	9	US-10-028-410-3	Sequence 3, Appl1
29	6	1.4	54	10	US-09-815-229-13	Sequence 13, Appl
30	6	1.4	56	10	US-09-864-761-41804	Sequence 41804, A
31	6	1.4	64	10	US-09-864-761-36407	Sequence 36407, A
32	6	1.4	73	12	US-10-062-254-16	Sequence 16, Appl
33	6	1.4	77	10	US-09-864-761-42061	Sequence 42061, A
34	6	1.4	78	10	US-09-864-761-38666	Sequence 38666, A
35	6	1.4	81	10	US-09-799-514-14	Sequence 14, Appl
36	6	1.4	86	9	US-09-878-380-1	Sequence 2, Appl1
37	6	1.4	86	9	US-10-028-410-2	Sequence 35, Appl
38	6	1.4	90	10	US-09-887-586A-35	Sequence 35, Appl
39	6	1.4	90	10	US-09-903-012-35	Sequence 46089, A
40	6	1.4	91	10	US-09-864-761-46089	Sequence 5022, Ap
41	6	1.4	91	10	US-09-815-242-10688	Sequence 10688, A
42	6	1.4	91	10	US-09-815-242-10688	Sequence 4, Appl1
43	6	1.4	96	9	US-09-947-563-4	Sequence 5, Appl1
44	6	1.4	96	9	US-09-947-563-5	Sequence 18, Appl
45	6	1.4	96	12	US-10-062-234-18	

ALIGNMENTS

RESULT 1
US-09-764-869-1013
; Sequence 1913, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764, 869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1013
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (61)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (74)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-869-1013
Query Match
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 VSLSLTL 9
Db 44 VSLSLTL 50
RESULT 2
US-09-789-919-42
; Sequence 42, Application US/09789919
; Patent No. US20020064855A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Thor
; APPLICANT: Moore, Kateri

;; TITLE OF INVENTION: GENES THAT REGULATE HEMATOPOIETIC BLOOD FORMING STEM
;; TITLE OF INVENTION: CELLS AND USES THEREOF
;; FILE REFERENCE: 2275-1-005
;; CURRENT APPLICATION NUMBER: US/09/789,919
;; CURRENT FILING DATE: 2001-02-21
;; NUMBER OF SEQ ID NOS: 96
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 42
;; LENGTH: 158
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-789-919-42

Query Match 1.6%; Score 7; DB 10; Length 158;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 TPSSHEAK 218
DB 11 TPSSHEAK 17

RESULT 3
US-09-098-079-14
; Sequence 14, Application US/09098079
; Patent No. US20020064773A1
; GENERAL INFORMATION:
; APPLICANT: Heirnstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Cleveland, William
; APPLICANT: Fahy, Eoin F. E.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
; TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,079
; FILING DATE: 15-JUN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 660088.416
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-098-079-14

Query Match 1.6%; Score 7; DB 10; Length 347;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LTLSTLS 14
DB 155 LTLSTLS 161

RESULT 4
US-09-773-882-2
; Sequence 2, Application US/09773882
; Patent No. US20020106769A1
; GENERAL INFORMATION:
; APPLICANT: Omura, Mitsuo
; APPLICANT: Inagaki, Tomoko
; APPLICANT: Matsumoto, Ryoji
; APPLICANT: Moriguchi, Takaya
; APPLICANT: Hasegawa, Shin
; APPLICANT: Suhayda, Charles
; TITLE OF INVENTION: UDP-D-Glucose:Limonoil Glucosyltransferase
; FILE REFERENCE: 0119.98
; CURRENT APPLICATION NUMBER: US/09/773,882
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-021179
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Citrus unshiu
US-09-773-882-2

Query Match 1.6%; Score 7; DB 10; Length 511;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 AFVDEVR 38
DB 459 AFVDEVR 465

RESULT 5
US-09-773-882-11
; Sequence 11, Application US/09773882
; Patent No. US20020106769A1
; GENERAL INFORMATION:
; APPLICANT: Omura, Mitsuo
; APPLICANT: Inagaki, Tomoko
; APPLICANT: Matsumoto, Ryoji
; APPLICANT: Moriguchi, Takaya
; APPLICANT: Hasegawa, Shin
; APPLICANT: Suhayda, Charles
; TITLE OF INVENTION: UDP-D-Glucose:Limonoil Glucosyltransferase
; FILE REFERENCE: 0119.98
; CURRENT APPLICATION NUMBER: US/09/773,882
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-021179
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Citrus unshiu
US-09-773-882-11

Query Match 1.6%; Score 7; DB 10; Length 511;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 AFVDEVR 38
DB 459 AFVDEVR 465

RESULT 6
US-09-815-242-11029
; Sequence 11029, Application US/09815242

Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11029
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-11029

Query Match 1.6%; Score 7; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 168 KQFPLS 174
DB 434 KQFPLS 440

RESULT 7
US-09-825-144-2
; Sequence 2, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Mathias Krause
; APPLICANT: Antonio S. Sechi
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Weiland
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 783
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-144-2

Query Match 1.6%; Score 7; DB 10; Length 783;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 268 NSRPFRV 274
DB 17 NSRPFRV 23

RESULT 8
US-09-825-144-4
; Sequence 4, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Mathias Krause
; APPLICANT: Antonio S. Sechi
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Weiland
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-144-4

Query Match 1.6%; Score 7; DB 10; Length 829;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 268 NSRPFRV 274
DB 17 NSRPFRV 23

RESULT 9
US-09-947-770-20
; Sequence 20, Application US/09947770
; Patent No. US20020068715A1
; GENERAL INFORMATION:
; APPLICANT: Steilman, Lawrence
; APPLICANT: Ruiz, Pedro
; APPLICANT: Garren, Hideki
; TITLE OF INVENTION: DNA Vaccination for Treatment of
; FILE REFERENCE: STAN123CIP
; CURRENT APPLICATION NUMBER: US/09/947,770
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/06233
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/267,590
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: insulin A (7-21) peptide
US-09-947-770-20

Query Match 1.4%; Score 6; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 LYOLEN 375
DB 7 LYOLEN 12

RESULT 10
US-09-732-561-23
; Sequence 23, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
; APPLICANT: Thomma, Bart
; APPLICANT: Terras, Frank
; APPLICANT: Penninckx, Irls
; APPLICANT: Manners, John
; APPLICANT: Kazan, Kemal
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Ag Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/202,638
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/01672
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: PPD 50165/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-732-561-23
; Query Match 1.4%; Score 6; DB 10; Length 17;
; Best Local Similarity 100.0%; Pred. No. 18;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 415 GYGSL 420
DB 11 GYGSL 16
RESULT 11
US-09-947-563-1
; Sequence 1, Application US/09947563
; Patent No. US20020156234A1
; GENERAL INFORMATION:
; APPLICANT: Rubroder, Franz-Josef
; APPLICANT: Keller, Reinhold
; TITLE OF INVENTION: Improved process for obtaining
; INSULIN precursors having correctly bonded cystine bridges
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farrahaw, Garrett &
; Dunnet
; STREET: 1300 I Street, N.W.

; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/947,563
; FILING DATE: 07-Sep-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/134,836
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie McDonnell
; REGISTRATION NUMBER: 34,872
; REFERENCE/DOCKET NUMBER: 02481.1600-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..21
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-947-563-1
; Query Match 1.4%; Score 6; DB 9; Length 21;
; Best Local Similarity 100.0%; Pred. No. 22;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 370 LYQLEN 375
DB 13 LYQLEN 18
RESULT 12
US-09-947-563-7
; Sequence 7, Application US/09947563
; Patent No. US20020156234A1
; GENERAL INFORMATION:
; APPLICANT: Rubroder, Franz-Josef
; APPLICANT: Keller, Reinhold
; TITLE OF INVENTION: Improved process for obtaining
; INSULIN precursors having correctly bonded cystine bridges
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farrahaw, Garrett &
; Dunnet
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/947,563
; FILING DATE: 07-Sep-2001


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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/134,836
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Leslie McDowell
REGISTRATION NUMBER: 34,872
REFERENCE/DOCKET NUMBER: 02481.1600-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: Protein
LOCATION: 1..21
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-947-563-7

Query Match
Best Local Similarity 1.4%; Score 6; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 LVOLEN 375
Db 13 LVOLEN 18

RESULT 13
US-09-853-844-1
; Sequence 1, Application US/09853844
; Patent No. US20020013269A1
; GENERAL INFORMATION:
; APPLICANT: Baltschmidt, Per
; TITLE OF INVENTION: Human Insulin Analogues
; FILE REFERENCE: 3343.270-US
; CURRENT APPLICATION NUMBER: US/09/853,844
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 08/965,221
; PRIOR FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: 08/531,842
; PRIOR FILING DATE: 1995-09-21
; PRIOR APPLICATION NUMBER: 08/275,196
; PRIOR FILING DATE: 1994-07-14
; PRIOR APPLICATION NUMBER: 07/976,805
; PRIOR FILING DATE: 1992-11-16
; PRIOR APPLICATION NUMBER: 07/453,445
; PRIOR FILING DATE: 1989-12-20
; PRIOR APPLICATION NUMBER: 07/416,218
; PRIOR FILING DATE: 1989-10-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-853-844-1

Query Match
Best Local Similarity 1.4%; Score 6; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 LVOLEN 375
Db 13 LVOLEN 18
```

```
RESULT 14
US-09-815-229-1
; Sequence 1, Application US/09815229
; Patent No. US20020058614A1
; GENERAL INFORMATION:
; APPLICANT: Filvaroff, Ellen H.
; APPLICANT: Okumu, Franklin W.
; TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGEOUS DISORDERS
; FILE REFERENCE: P1786R1US
; CURRENT APPLICATION NUMBER: US/09/815,229
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/192,103
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-815-229-1

Query Match
Best Local Similarity 1.4%; Score 6; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 LVOLEN 375
Db 13 LVOLEN 18

RESULT 15
US-10-066-151-102
; Sequence 102, Application US/10066151
; Patent No. US2002013300A1
; GENERAL INFORMATION:
; APPLICANT: Hogan, Patrick G.
; APPLICANT: Rao, Anjana
; TITLE OF INVENTION: SPECIFIC INHIBITORS OF NEAT ACTIVATION
; TITLE OF INVENTION: BY CALCINEURIN AND THEIR USE IN TREATING IMMUNE-RELATED
; FILE REFERENCE: 10861-004002
; CURRENT APPLICATION NUMBER: US/10/066,151
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 09/248,620
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/074,467
; PRIOR FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide containing the
; OTHER INFORMATION: SPRIETPS amino acid sequence
US-10-066-151-102

Query Match
Best Local Similarity 1.4%; Score 6; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 TPSSHA 217
Db 15 TPSSHA 20

Search completed: November 12, 2002, 11:49:39
Job time : 6.75 secs
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:45 ; Search time 7.5 Seconds

(Without alignments)
2444.338 Million cell updates/sec

Title: US-09-787-083-2

Perfect score: 442

Sequence: 1 MKVSLSTLSTLSTLSCFAI...YMHKATSPGVGLMNDMMGL 442

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	1.8	286	1	PAL_KLEPN
2	8	1.8	1396	1	VLPF_BPT5
3	7	1.6	197	1	TBA_PLAYO
4	7	1.6	212	1	PRL_ICTPU
5	7	1.6	240	1	TBA_OCTVU
6	7	1.6	270	1	T304_MTCPU
7	7	1.6	273	1	ILVE_THEMA
8	7	1.6	322	1	MIAA_PSEPU
9	7	1.6	326	1	SPI_BACBR
10	7	1.6	342	1	FIAD_METJA
11	7	1.6	342	1	V755_METJA
12	7	1.6	347	1	NU2M_CAPHI
13	7	1.6	347	1	NU2M_HUMAN
14	7	1.6	347	1	NU2M_PANTR
15	7	1.6	347	1	NU2M_PONPA
16	7	1.6	347	1	NU2M_SHEEP
17	7	1.6	423	1	AMT_AQUAE
18	7	1.6	444	1	TBA_ONCKE
19	7	1.6	448	1	TBA4_HUMAN
20	7	1.6	448	1	TBA5_CHICK
21	7	1.6	449	1	TBA2_DROME
22	7	1.6	449	1	TBAE_PHYPO
23	7	1.6	449	1	TBAE_PHYPO
24	7	1.6	449	1	TBA_XENIA
25	7	1.6	450	1	TBA4_HUMAN
26	7	1.6	450	1	TBA4_HUMAN
27	7	1.6	450	1	TBA4_HUMAN
28	7	1.6	451	1	TBA3_HUMAN
29	7	1.6	451	1	TBA3_HUMAN
30	7	1.6	451	1	TBA_TORMA
31	7	1.6	451	1	TBA_TORMA
32	7	1.6	513	1	ATPA_HAEIN
33	7	1.6	513	1	ATPA_HAEIN

34	7	1.6	536	1	601M_BUCAP	P29431	buchnera ap
35	7	1.6	544	1	GPI0_DICDI	006885	dicyostell
36	7	1.6	567	1	GPV_RAT	008770	rattus norv
37	7	1.6	610	1	FIMB_DICDI	P54680	halocystell
38	7	1.6	635	1	DNAR_HAIMA	001100	halocystell
39	7	1.6	681	1	CAO2_HUMAN	099424	homo sapien
40	7	1.6	768	1	YB23_HUMAN	091177	homo sapien
41	7	1.6	783	1	YFB_HUMAN	015117	homo sapien
42	7	1.6	824	1	TG37_MOUSE	061371	mus musculu
43	7	1.6	862	1	AXN1_HUMAN	015169	homo sapien
44	7	1.6	947	1	LKTA_PASSP	P55123	pasteurella
45	7	1.6	1026	1	VG37_BPT4	P03744	bacterioph

ALIGNMENTS

RESULT 1	ID	Pal_KLEPN	STANDARD	PRT	286 AA
AC	P37446				
DT	01-OCT-1994 (Rel. 30, Created)				
DT	01-OCT-1994 (Rel. 30, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	Phospholipase A1 precursor (EC 3.1.1.32) (Detergent-resistant				
DE	phospholipase A) (DR-phospholipase A) (Phosphatidylcholine 1-				
DE	acylglycerolase) (outer membrane phospholipase A) (OM PLA).				
GN	PLDA.				
OS	Klebsiella pneumoniae.				
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;				
OC	Klebsiella.				
OX	NCBI_TaxID-573;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-94131966; PubMed-8300539;				
RA	Brok R.G.P.M., Brinkman E., van Boxtel R., Bekkers A.C.A.P.,				
RA	Verheij H.M., Tomassen J.;				
RT	Molecular characterization of enterobacterial plda genes encoding				
RT	outer membrane phospholipase A.*;				
RL	J. Bacteriol. 176:861-870(1994).				
CC	- FUNCTION: HYDROLYSIS OF PHOSPHATIDYLCHOLINE WITH PHOSPHOLIPASE				
CC	A2 (EC 3.1.1.4) AND PHOSPHOLIPASE A1 (EC 3.1.1.32) ACTIVITIES.				
CC	- CATALYTIC ACTIVITY: Phosphatidylcholine + H2O -> 1-				
CC	acylglycerophosphocholine + a fatty acid anion.				
CC	- CATALYTIC ACTIVITY: Phosphatidylcholine + H2O -> 2-				
CC	acylglycerophosphocholine + a fatty acid anion.				
CC	- COFACTOR: REQUIRES CALCIUM IONS FOR ACTIVITY.				
CC	- SUBCELLULAR LOCATION: OUTER MEMBRANE; ONE OF THE VERY FEW ENZYMES				
CC	LOCATED THERE.				
CC	-----				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL: X76901; CAA54223.1; -				
DR	PIR: B36971; B36971.				
DR	PIR: S40129; S40129.				
DR	HSSP: P00631; 10D6.				
DR	InterPro: IPR003187; PLA1.				
DR	PIR: P02253; PLA1.				
DR	PRINTS: PR01486; PHPLIPASEA1.				
KW	Hydrolase; Lipid degradation; Outer membrane; Signal; Calcium.				
FT	STGNL				
FT	CHAIN				
FT	ACT SITE				
FT	SEQUENCE				
FT	286 AA; 32544 MW; 3E39F863085108A3 CRC64;				
FT	1.8%; Score 8; DB 1; Length 286;				
FT	Best Local Similarity 100.0%; Pred. No. 1.5;				

Matches 8; Conservative 0; Mismatches : 0; Indels 0; Gaps 0;

OY 431 GVGMLND 438.
 |||||
 RN
 DB 277 GVGMLND 284

RESULT 2

VTFF_BPT5 STANDARD; PRT: 1396 AA.
 AC P13390: Q48502;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE L-shaped tail fiber protein (LTF protein).
 GN LTF.
 OS Bacteriophage T5.
 CC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 CC T5-like viruses.
 OX NCBI_TaxID=10726;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95309401; PubMed=7789514;
 RA Kaliman A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.,
 RA Kryukov V.M.;
 RT "The nucleotide sequence of the bacteriophage T5 ltf gene.";
 RL FEBS Lett. 366:46-48(1995).
 [2]
 RP SEQUENCE FROM N.A.
 RA Kaliman A.V.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE=88289370; PubMed=3267228;
 RA Kaliman A.V., Kryukov V.M., Bayev A.A.;
 RT "The nucleotide sequence of bacteriophage T5 DNA at the region
 between early and late genes.";
 RL Nucleic Acids Res. 16:6230-6230(1988).
 CC -1- FUNCTION: NONESSENTIAL PROTEIN THAT MEDIATES BINDING TO THE
 POLYMANNOSE O ANTIGEN.
 CC -----
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 CC -----
 DR EMBL: X69460; CAA49220.1; -;
 DR EMBL: AJ001191; CAA04591.1; -;
 DR PIR: S01982; S01982.
 KW Late protein.
 FT CONFLICT 986 986 V -> A (IN REF. 2).
 FT SEQUENCE 1396 AA; 147989 MW; 18CD2192F65FFFC1 CRC64;

Query Match 1.8%; Score 8; DB 1; Length 1396;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 QSATOSAS 61
 |||||
 DB 87 QSATOSAS 94

RESULT 3

TBA_PLAYO STANDARD; PRT: 197 AA.
 AC P12543;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Tubulin alpha chain (Fragment).

OS Plasmodium berghei yoelli.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5862;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=89014607; PubMed=2459618;
 RA Akella R., Arasu P., Valdaya A.B.;
 RT "Molecular clones of alpha-tubulin genes of Plasmodium yoelli reveal
 an unusual feature of the carboxy terminus.";
 RL Mol. Biochem. Parasitol. 30:165-174(1988).
 CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
 CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
 CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
 CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
 CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: M29816; AAA29779.1; -;
 DR PIR: A54506; A54506.
 DR InterPro: IPR000217; Tubulin.
 DR InterPro: IPR003008; Tubulin_Fts2.
 DR Pfam: PF00091; tubulin; 1.
 DR PROSITE: PS00227; TUBULIN; PARTIAL.
 KW Microtubules; GTP-binding.
 FT NON_TER 1
 FT SEQUENCE 197 AA; 22111 MW; 4DAAF199CC6CD319 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred. No. 13;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 ITRKRSI 120
 |||||
 DB 82 ITRKRSI 88

RESULT 4

PRL_ICTPU STANDARD; PRT: 212 AA.
 AC P51904: Q91819;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Prolactin precursor (PRL).
 GN PRL.
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OX NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RA Tang Y.;
 RT "A study on the channel catfish (Ictalurus punctatus) growth hormone
 RT gene family: structures of growth hormone and prolactin genes and
 RT somatolactin cDNA, their evolutionary implications and expression in
 RT the pituitary gland.";
 RL Thesis (1993), University of Maryland, U.S.A.
 RN [2]
 RP SEQUENCE OF 27-212 FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=93364578; PubMed=1308206;
 RA Watanabe K., Igarashi A., Noso T., Chen T.T., Dunham R.A.,
 RA Kawachi H.;
 RT "Chemical identification of catfish growth hormone and prolactin.";

```

RL Mol. Biol. Biotechnol. 1:239-249(1992).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PITUITARY GLANDS.
CC -1- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
CC -----
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CC -----
DR EMBL: AF267990; AAF82287.1; -.
DR HSSP: 028632; 1AN3.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF00103; hormone; 2.
DR PRINTS: PR00836; SOMATOTROPIN.
DR PROSITE: PS00266; SOMATOTROPIN_1; 1.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
KM Hormone; pituitary; signal.
FT SIGNAL 1 26
FT CHAIN 27 212
FT DISULFID 71 185 BY SIMILARITY.
FT DISULFID 202 212 BY SIMILARITY.
FT CONFLICT 91 91 G -> S (IN REF. 2).
FT CONFLICT 128 128 T -> S (IN REF. 2).
FT CONFLICT 203 203 D -> R (IN REF. 2).
SQ SEQUENCE 212 AA; 23365 MW; 073FB/FBIDA573BE CRC64;

Query Match
Best Local Similarity 1.6%; Score 7; DB 1; Length 212;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NDIGQDN 47
DB 166 NDIGQDN 172

RESULT 5
TBA_OCTVU STANDARD; PRT; 240 AA.
AC P24635;
DR 01-MAR-1992 (Rel. 21, Created)
DR 01-MAR-1992 (Rel. 21, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tubulin alpha chain (Fragment).
OS Octopus vulgaris (Octopus).
CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
CC Incirrata; Octopodidae; Octopus.
CC NCBL_TaxID=6645;
RN NCBL_TaxID=6645;
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RA Zinov'Eva R.D., Alelnikova K.S., Tomarev S.I.;
RT tubulin of the octopus eye lens.
RL tubulin of the octopus eye lens.
DR DOKI. Akad. Nauk SSSR 302:462-467(1988).
CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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CC -----
EMBL: X15845; CAA33844.1; -.

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DR PIR: A61544; A61544.
DR InterPro: IPR000217; Tubulin.
DR InterPro: IPR003008; Tubulin_FtsZ.
DR Pfam: PF00091; tubulin; 1.
DR PROSITE: PS00227; TUBULIN; PARTIAL.
KM Microtubules; GTP-binding.
FT NON_TER 1 1
FT SITE 240 240 INVOLVED IN POLYMERIZATION.
SQ SEQUENCE 240 AA; 26961 MW; 13BB3A1F740F2416 CRC64;

Query Match
Best Local Similarity 1.6%; Score 7; DB 1; Length 240;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 IKTKRSI 120
DB 124 IKTKRSI 130

RESULT 6
Y304_MYCPN STANDARD; PRT; 270 AA.
AC P75355;
DR 01-NOV-1997 (Rel. 35, Created)
DR 01-NOV-1997 (Rel. 35, Last sequence update)
DR 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical ABC transporter ATP-binding protein MG304 homolog
DE (A05_orf270L).
GN MPN433 OR MP408.
OS Mycoplasma pneumoniae.
CC Bacteria; Firmicutes; Molluscites; Mycoplasmataceae; Mycoplasma.
CC NCBL_TaxID=2104;
RN NCBL_TaxID=2104;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RA MEDLINE=97105885; PubMed=8948633;
RA Himmelfreich R., Hlbert H., Plagens H., Pirkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae."
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
CC -----
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CC -----
CC EMBL: AE000040; AAB96056.1; -.
DR InterPro: IPR003593; AAA_Artpase.
DR InterPro: IPR003439; ABC_transporter.
DR Pfam: PF000005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KM Hypothetical protein: ATP-binding; Transport; Complete proteome.
FT NP_BIND 36 43 ATP (POTENTIAL).
SQ SEQUENCE 270 AA; 30770 MW; 6512640E4BC051B4 CRC64;

Query Match
Best Local Similarity 1.6%; Score 7; DB 1; Length 270;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 KOFTPLS 174
DB 125 KOFTPLS 131

RESULT 7
ILVE_THEMA

```

ID ILVE_THEME STANDARD; PRT; 273 AA.
AC P74921;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable branched-chain amino acid aminotransferase (EC 2.6.1.42)
DE (BCAT).
GN ILVE OR TM0831.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
OC Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Halt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima."
RL Nature 393:323-329(1999).
RN [2]
RP SEQUENCE OF 68-273 FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=97017137; PubMed=8863738;
RA Guipaud O., Labedan B., Forterre P.;
RT "A gyrB-like gene from the hyperthermophilic bacterium Thermotoga
maritima."
RL Gene 174:121-128(1996).
CC -1- FUNCTION: Acts on leucine, isoleucine and valine (By similarity).
CC -1- CATALYTIC ACTIVITY: L-leucine + 2-oxoglutarate = 4-methyl-2-
oxopentanoate + L-glutamate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: Valine and isoleucine biosynthesis.
CC -1- SIMILARITY: BELONGS TO CLASS-IV OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
CC -----
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CC -----
DR EMBL: AE001750; A035913.1; -.
DR EMBL: U49692; AAC4497.1; -.
DR HSSP: P00510; 1A3G.
DR TIGR: TM0831; -.
DR InterPro: IPR001544; AminoTran_4.
DR Pfam: PF01063; AminoTran_4; 1.
DR ProDom: PD001961; AminoTran_4; 1.
DR PROSITE: PS00770; AA_TRANSFERRER_CLASS_4; 1.
KW Transferrase; AminoTransferase; Branched-chain amino acid biosynthesis;
KW Pyridoxal phosphate; Complete proteome.
FT CONFLICT 77 A->R (IN REF. 2).
SQ SEQUENCE 273 AA; 31158 MW; 2162B705612E90E3 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 273;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 172 PLSTSPD 178
Db 61 PLSTSPD 67

RESULT 8
MIAA_PSEPU

ID MIAA_PSEPU STANDARD; PRT; 322 AA.
AC O30762;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (IPP
transferase) (isopentenyl-diphosphate:tRNA isopentenyltransferase)
DE (IPPTase).
GN MIAA.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M;
RA Olekhovich I.N., Gusslin G.N.;
RT "Attenuation of the Pseudomonas putida trpE and trpGDC genes."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE FIRST STEP IN THE BIOSYNTHESIS OF
2-METHYLTHIO-N6-(DELTA(2)-ISOPENTENYL)-ADENOSINE (MS121i[6A])
ADJACENT TO THE ANTICODON OF SEVERAL TRNA SPECIES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA - diphosphate +
tRNA containing 6-isopentenyladenosine.
CC -1- SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
CC -----
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CC -----
DR EMBL: AF016312; AAB69443.1; -.
DR InterPro: IPR002627; IPPT.
DR Pfam: PF01715; IPPT; 1.
DR ProDom: PD004674; IPPT; 1.
DR TIGRFAMs: TIGR00174; MIAA; 1.
KW Transferase; Nucleotidyltransferase; tRNA processing; ATP-binding.
FT NP_BIND 12 19 ATP (POTENTIAL).
SQ SEQUENCE 322 AA; 35488 MW; D1AA81A2D7B32F6A CRC64;

Query Match 1.6%; Score 7; DB 1; Length 322;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 FVDEVRS 39
Db 231 FVDEVRS 237

RESULT 9
SPL_BACBR
ID SPL_BACBR STANDARD; PRT; 326 AA.
AC P43131;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Protease inhibitor precursor (BBRI).
OS Bacillus brevis.
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
OX NCBI_TaxID=1193;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-32; 104-112 AND 122-136.
RC STRAIN=HPD31;
RX MEDLINE=92304060; PubMed=1610177;
RA Shiga Y., Hasegawa K., Tsuboi A., Yamagata H., Uda K.S.;
RT "Characterization of an extracellular protease inhibitor of Bacillus
brevis HPD31 and nucleotide sequence of the corresponding gene."
RL Appl. Environ. Microbiol. 58:525-531(1992).
CC -1- FUNCTION: SHOWS INHIBITORY ACTIVITY TOWARDS SERINE PROTEASES, SUCH
AS TRYPSIN, CHYMOTRYPSIN, AND SUBTILISIN. MAY FORM A TRYPSIN-

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CC INHIBITOR COMPLEX IN A MOLAR RATIO OF 1:1. IT IS HEAT RESISTANT AT
CC NEUTRAL AND ACIDIC PHs.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: MAY UNDERGO ACTIVATION AFTER SECRETION. IT IS PRODUCED
CC EXTRACELLULARLY IN MULTIPLE FORMS HAVING AT LEAST THREE DIFFERENT
CC MOLECULAR WEIGHTS (BBRP1-A, -B, AND -C).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D10696; BAA01538.1;
KW Serine protease inhibitor; Protease inhibitor; Signal; Repeat.
FT SIGNAL 1 24
FT CHAIN 25 326 SERINE PROTEASE INHIBITOR.
FT CHAIN 104 326 SERINE PROTEASE INHIBITOR-C.
FT CHAIN 104 ? SERINE PROTEASE INHIBITOR-B (POTENTIAL).
FT DOMAIN 122 326 SERINE PROTEASE INHIBITOR-A.
FT REPEAT 177 304 CONTAINS TWO APPROXIMATE REPEATS.
FT REPEAT 177 208 1.
FT REPEAT 272 304 2.
SQ SEQUENCE 326 AA; 35100 MW; 1C0456ABFA912F77 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 326;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 30 PVAEYDE 36
    |||||
Db 119 PVAEYDE 125

RESULT 10
FLAD_METJA STANDARD; PRT; 342 AA.
ID FLAD_METJA
AC Q58305;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative flagella-related protein D.
GN FLAD OR MJ0895.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kierulff A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reisch C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodok A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RT Science 273:1058-1073(1996).
RL -1- SIMILARITY: STRONG. TO M.VOLTAE FLAD, ALSO TO FLAE.
CC -----
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CC -----
DR EMBL; U67533; AAB98898.1;
DR TIGR; MJ0895;
KW Flagella; Complete proteome.
SQ SEQUENCE 342 AA; 39950 MW; B384DDE1775566C CRC64;

Query Match 1.6%; Score 7; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 356 PDILDY 362
    |||||
Db 255 PDILDY 261

RESULT 11
Y755_METJA STANDARD; PRT; 342 AA.
ID Y755_METJA
AC Q58165;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0755 precursor.
GN MJ0755.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kierulff A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reisch C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodok A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RT Science 273:1058-1073(1996).
RL -1- SIMILARITY: STRONG. TO M.VOLTAE FLAD, ALSO TO FLAE.
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CC -----
DR EMBL; U67521; AAB9748.1;
DR TIGR; MJ0755;
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 342 HYPOTHETICAL PROTEIN MJ0755.
SQ SEQUENCE 342 AA; 38778 MW; BD25220A7EAD85C CRC64;

Query Match 1.6%; Score 7; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 76 YTTALEN 82
    |||||
Db 90 YTTALEN 96

RESULT 12
NU2M_CAPHI STANDARD; PRT; 347 AA.
ID NU2M_CAPHI
AC Q36346;
DT 01-NOV-1997 (Rel. 35, Created)

```

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
 GN MTND2 OR ND2.
 OS Capra hircus (Goat).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Dove P., Mann W., Hecht W.;
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 CC - CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC - SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC - SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
 CC -----
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 CC -----
 CC EMBL; X72965; CAAS1468.1; -
 DR InterPro: IPR003917; NADHub_oxred2.
 DR InterPro: IPR001750; Oxidored_q1.
 DR Pfam: PF00361; oxidored_q1; 1.
 DR PRINTS: PR01436; NADHHCNASE2.
 DR Oxidoreductase; NAD: Ubiquinone; Mitochondrion; Transmembrane.
 SQ SEQUENCE 347 AA; 39136 MW; 6129CF9080475E CRC64;

Query Match 1.68; Score 7; DB: 1; Length 347;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LTLSTLS 14
 |||||
 Db 155 LTLSTLS 161

RESULT 13
 NU2M_HUMAN STANDARD: PRT: 347 AA.
 AC P03851: Q34769: Q9TGI0: Q9TGI1: Q9TGI2: Q9TGI3: Q9TGI4:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
 GN MTND2 OR ND2.
 OS Homo sapiens (Human).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=81173052; PubMed=7219534;
 RA Anderson S., Bankier A.T., Barrell B.G., de Bruijn M.H.L.,
 RA Coulson A.R., Drouin J., Eperon I.C., Nierlich D.P., Roe B.A.,
 RA Sanger F., Scheiler P.H., Smith A.J.H., Staden R., Young I.G.;
 RT "Sequence and organization of the human mitochondrial genome.";
 RL Nature 290:457-465(1981).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=81170577; PubMed=6260957;
 RA Sanger F., Coulson A.R., Barrell B.G., Smith A.J.H., Roe B.A.;
 RT "Cloning in single-stranded bacteriophage as an aid to rapid DNA
 sequencing.";

RL J. Mol. Biol. 143:161-178(1980).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS V-69; S-88; D-150; M-237; T-265;
 RP T-278; V-265 AND A-333.
 RX MEDLINE=98133898; PubMed=9475751;
 RA Wise C.A., Strahl M., Eastaugh S.;
 RT "Departure from neutrality at the mitochondrial NADH dehydrogenase
 RL subunit 2 gene in humans, but not in chimpanzees.";
 RN Genetics 148:409-421(1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS ILE-43; LEU-325 AND THR-331.
 RC TISSUE=Placenta;
 RX MEDLINE=95132634; PubMed=7530363;
 RA Horai S., Hayasaka K., Kondo R., Tsugane K., Takahata N.;
 RT "Recent African origin of modern humans revealed by complete sequences
 RL of hominid mitochondrial DNAs.";
 RN Proc. Natl. Acad. Sci. U.S.A. 92:532-536(1995).
 RN [5]
 RP IDENTIFICATION OF PROTEIN.
 RX MEDLINE=85188293; PubMed=3921850;
 RA Chomyn A., Mariotti P., Cleeter M.W.J., Ragan C.I., Matsuno-Yagi A.,
 RA Hatell Y., Doellittle R.F., Attridge G.;
 RT "Six unidentified reading frames of human mitochondrial DNA encode
 RL components of the respiratory-chain NADH dehydrogenase.";
 RN Nature 314:592-597(1985).
 RN [6]
 RP VARIANT LHON ASP-150.
 RX MEDLINE=91144615; PubMed=1900003;
 RA Johns D.R., Berman J.;
 RT "Alternative, simultaneous complex I mitochondrial DNA mutations in
 RT Leber's hereditary optic neuropathy.";
 RL Biochem. Biophys. Res. Commun. 174:1324-1330(1991).
 RN [7]
 RP VARIANTS L-42; R-63; A-119; P-148; S-150; T-159 AND A-185.
 RX MEDLINE=92098084; PubMed=1757091;
 RA Marzuki S., Noer A.S., Lertit P., Thyagarajan D., Kapsa R.,
 RA Utthanaphol P., Byrne E.;
 RT "Normal variants of human mitochondrial DNA and translation products:
 RL the building of a reference data base.";
 RN Hum. Genet. 88:139-145(1991).
 RN [8]
 RP VARIANT LHON SER-259.
 RX MEDLINE=92120513; PubMed=1732158;
 RA Brown M.D., Voljavec A.S., Lott M.T., Torroni A., Yang C.C.,
 RA Wallace D.C.;
 RT "Mitochondrial DNA complex I and III mutations associated with
 RT Leber's hereditary optic neuropathy.";
 RL Genetics 130:163-173(1992).
 RN [9]
 RP VARIANT AD SER-331.
 RX MEDLINE=92118019; PubMed=1370613;
 RA Lin F.-H., Lin R., Wisniewski H.M., Hwang Y.-W., Grundke-Iqbal I.,
 RA Healy-Louie G., Iqbal K.;
 RT "Detection of point mutations in codon 331 of mitochondrial NADH
 RL dehydrogenase subunit 2 in Alzheimer's brains.";
 RL Biochem. Biophys. Res. Commun. 182:238-246(1992).
 RN [10]
 RP VARIANT THR-57.
 RX MEDLINE=98127994; PubMed=9461455;
 RA Rieder M.J., Taylor S.L., Tobe V.O., Nickerson D.A.;
 RT "Automating the identification of DNA variations using quality-based
 RT fluorescence re-sequencing: analysis of the human mitochondrial
 RL genome.";
 RL Nucleic Acids Res. 26:967-973(1998).
 CC - CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC - SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC - DISEASE: DEFECTS IN MTND2 ARE ONE OF THE CAUSES OF LEBER'S
 CC HEREDITARY OPTIC NEUROPATHY (LHON), A MATERNALLY INHERITED DISEASE
 CC RESULTING IN ACUTE BILATERAL BLINDNESS DUE TO RETINAL DEGENERATION
 CC PREDOMINANTLY IN YOUNG MEN. CARDIAC CONDUCTION DEFECTS AND
 CC NEUROLOGICAL DEFECTS HAVE ALSO BEEN DESCRIBED. RESULTING IN OPTIC
 CC NERVE DEGENERATION AND CARDIAC DYSRHYTHMIA.

CC -!- DISEASE: DEFECTS IN MTND2 COULD BE ASSOCIATED WITH ALZHEIMER'S
 CC DISEASE (AD).
 CC -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
 CC -----
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 CC -----
 DR EMBL: J01415; AAB58944.1; -;
 DR EMBL: V00662; CAA24027.1; -;
 DR EMBL: M10546; BAA07291.1; -;
 DR EMBL: D38112; BAA07291.1; -;
 DR EMBL: AF014882; AAC25441.1; -;
 DR EMBL: AF014884; AAC25443.1; -;
 DR EMBL: AF014885; AAC25444.1; -;
 DR EMBL: AF014887; AAC25446.1; -;
 DR EMBL: AF014889; AAC25448.1; -;
 DR EMBL: AF014890; AAC25449.1; -;
 DR EMBL: AF014891; AAC25450.1; -;
 DR EMBL: AF014892; AAC25451.1; -;
 DR EMBL: AF014895; AAC25454.1; -;
 DR EMBL: AF014896; AAC25455.2; -;
 DR EMBL: AF014897; AAC25456.1; -;
 DR EMBL: AF014898; AAC25457.1; -;
 DR EMBL: AF014899; AAC25458.2; -;
 DR EMBL: AF014900; AAC25459.1; -;
 DR EMBL: AF014901; AAC25460.1; -;
 DR PIR: A00414; DHMUN2.
 DR Genew; HGNC:7456; MTND2.
 DR MIM: 502500; -;
 DR MIM: 516001; -;
 DR MIM: 535000; -;
 DR InterPro: IPR003917; NADHoxred2.
 DR InterPro: IPR001750; Oxidored_q1.
 DR Pfam: PF00361; Oxidored_q1; 1.
 DR PRINTS: PRO1436; NADHDHGNASE2.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane;
 KW Disease mutation; Leber's hereditary optic neuropathy;
 KW Alzheimer's disease; Polymorphism.
 FT VARIANT 42 42 P->L.
 FT VARIANT 43 43 /FTId-VAR_008590.
 FT VARIANT 57 57 V->I.
 FT VARIANT 57 57 /FTId-VAR_011348.
 FT VARIANT 63 63 I->T.
 FT VARIANT 63 63 /FTId-VAR_008591.
 FT VARIANT 69 69 O->R.
 FT VARIANT 69 69 /FTId-VAR_008592.
 FT VARIANT 88 88 I->V.
 FT VARIANT 88 88 /FTId-VAR_011349.
 FT VARIANT 119 88 N->S.
 FT VARIANT 119 119 /FTId-VAR_011350.
 FT VARIANT 148 148 T->A.
 FT VARIANT 148 148 /FTId-VAR_008593.
 FT VARIANT 150 150 S->P.
 FT VARIANT 150 150 /FTId-VAR_008594.
 FT VARIANT 159 159 N->D (IN LHON; SECONDARY MUTATION; DOES
 FT VARIANT 159 159 NOT SEEM TO DIRECTLY CAUSE THE DISEASE).
 FT VARIANT 185 185 /FTId-VAR_004755.
 FT VARIANT 185 185 N->S.
 FT VARIANT 185 185 /FTId-VAR_008595.
 FT VARIANT 185 185 I->T.
 FT VARIANT 237 237 /FTId-VAR_008596.
 FT VARIANT 237 237 T->A.
 FT VARIANT 237 237 /FTId-VAR_008597.
 FT VARIANT 259 259 /FTId-VAR_011351.
 FT VARIANT 259 259 G->S (IN LHON; RARE PRIMARY MUTATION).
 FT VARIANT 265 265 /FTId-VAR_004756.
 FT VARIANT 265 265 A->T.

FT VARIANT 265 265 /FTId-VAR_011352.
 FT VARIANT 265 265 A->V.
 FT VARIANT 278 278 /FTId-VAR_011353.
 FT VARIANT 278 278 I->T.
 FT VARIANT 325 325 /FTId-VAR_011354.
 FT VARIANT 325 325 F->L.
 FT VARIANT 331 331 /FTId-VAR_011355.
 FT VARIANT 331 331 A->S (IN AD).
 FT VARIANT 331 331 /FTId-VAR_004758.
 FT VARIANT 331 331 A->T.
 FT VARIANT 333 333 /FTId-VAR_004757.
 FT VARIANT 333 333 T->A.
 FT SEQUENCE 347 AA; 38961 MW; C06FD982317C3FE2D CRC64;
 SQ
 Query Match 1.6%; Score 7; DB 1; Length 347;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 LTLSTLS 14
 Db 155 LTLSTLS 161
 RESULT 14
 N02M_PANTR STANDARD; PRT; 347 AA.
 ID N02M_PANTR
 AC 021798;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
 GN MTND2 OR ND2.
 OS Pan troglodytes (Chimpanzee).
 OG Mitochondrion.
 OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98133898; PubMed=9475751;
 RA Wise C.A., Strahl M., Eastaugh S.;
 RT "Departure from neutrality at the mitochondrial NADH dehydrogenase
 RT subunit 2 gene in humans, but not in chimpanzees.";
 RL Genetics 148:409-421(1998).
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
 CC -----
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 DR EMBL: AF014908; AAC25467.1; -;
 DR EMBL: AF014909; AAC25468.1; -;
 DR EMBL: AF014910; AAC25469.1; -;
 DR EMBL: AF014911; AAC25470.1; -;
 DR EMBL: AF014912; AAC25471.1; -;
 DR EMBL: AF014913; AAC25472.1; -;
 DR EMBL: AF014914; AAC25473.1; -;
 DR EMBL: AF014915; AAC25474.1; -;
 DR EMBL: AF014916; AAC25475.1; -;
 DR EMBL: AF014917; AAC25476.1; -;
 DR EMBL: AF014918; AAC25477.1; -;
 DR EMBL: AF014919; AAC25478.1; -;
 DR EMBL: AF014920; AAC25479.1; -;
 DR EMBL: AF014921; AAC25480.1; -;
 DR InterPro: IPR003917; NADHoxred2.

DR InterPro: IPR001750; Oxidored_g1.
 DR Pfam: PF00361; Oxidored_g1; 1.
 DR PRINTS: PR01436; NADHDHGNASE2.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
 FT VARIANT 94 94 P -> S (IN STRAIN A-292).
 SQ SEQUENCE 347 AA; 39020 MW; 2E8269D105810D4E CRC64;

Query Match 1.6%; Score 7; DB 1; Length 347;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 LITSLIS 14
 DB 155 LITSLIS 161

RESULT 15
 NU2M_PONPA STANDARD; PRT; 347 AA.
 ID NU2M_PONPA
 AC P92691;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
 GN MTND2 OR ND2 OR NADH2.
 OS Pongo pygmaeus abelii (Sumatran orangutan).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pongo.
 OX NCBI_TaxID-9601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YN93-312;
 RX MEDLINE=97032590; PubMed=875856;
 RA Xu X., Arason U.;
 RT "The mitochondrial DNA molecule of Sumatran orangutan and a molecular
 proposal for two (Bornean and Sumatran) species of orangutan.";
 RL J. Mol. Evol. 43:431-437(1996).
 CC -1 CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1 SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
 CC -----
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 CC -----
 CC EMBL: X97707; CAA66284.1; -
 DR InterPro: IPR003917; NADhub_oxred2.
 DR InterPro: IPR001750; Oxidored_g1.
 DR Pfam: PF00361; Oxidored_g1; 1.
 DR PRINTS: PR01436; NADHDHGNASE2.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
 SQ SEQUENCE 347 AA; 38619 MW; 5388526466A2B93 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 347;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LITSLIS 14
 DB 155 LITSLIS 161

Search completed: November 12, 2002, 11:45:26
 Job time : 9.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:46 ; Search time 26.25 Seconds
(without alignments)
3469.441 Million cell updates/sec

Title: US-09-787-083-2

Perfect score: 442
Sequence: 1 MKVSLSTLSTLSTSCFAIIA.....YHNEATSRGVGLMDNMGL 442

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.rvirus:*
16: sp.bacteriaph:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	9	2.0	382	16	Q9K0U7
2	9	2.0	409	16	Q9K0U7
3	9	2.0	862	16	Q9J121
4	9	2.0	1432	10	Q9A162
5	8	1.8	227	17	Q8TUS3
6	8	1.8	299	10	Q9M268
7	8	1.8	306	16	Q9CL22
8	8	1.8	415	8	Q94ZC0
9	7	1.6	55	12	Q67608
10	7	1.6	68	16	Q9J2F7
11	7	1.6	72	12	Q9J2S4
12	7	1.6	72	12	Q9J2S5
13	7	1.6	95	12	Q9J2S3
14	7	1.6	96	12	Q9J2S8
15	7	1.6	100	3	Q12148
16	7	1.6	101	12	Q9J2S6

17	7	1.6	112	16	Q92HS2
18	7	1.6	122	16	Q9RU16
19	7	1.6	124	12	Q9J2S7
20	7	1.6	131	6	Q9GMD4
21	7	1.6	138	12	Q9J2Q7
22	7	1.6	142	16	Q8RAS3
23	7	1.6	147	5	Q36035
24	7	1.6	158	16	Q929C1
25	7	1.6	164	16	Q9J2H4
26	7	1.6	169	16	Q9J2A7
27	7	1.6	183	16	Q8YMM0
28	7	1.6	185	17	Q97UY1
29	7	1.6	186	10	Q9J2X9
30	7	1.6	189	13	Q9DPT2
31	7	1.6	198	4	Q9BUX3
32	7	1.6	200	5	Q8T2L3
33	7	1.6	212	13	Q902N5
34	7	1.6	214	5	Q9VTR5
35	7	1.6	216	2	Q9X6H5
36	7	1.6	218	2	Q9R14
37	7	1.6	219	5	Q17594
38	7	1.6	220	5	Q9XCK1
39	7	1.6	220	5	Q36036
40	7	1.6	221	12	Q65002
41	7	1.6	227	5	Q9BME4
42	7	1.6	233	6	Q9M2B0
43	7	1.6	233	16	Q8YH08
44	7	1.6	236	13	Q9DPS8
45	7	1.6	264	12	Q85260

ALIGNMENTS

RESULT 1
ID Q9K0U7 PRELIMINARY; PRT; 382 AA.
AC Q9K0U7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Phospholipase A1, putative.
GN NMB0464.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-MC58 / SEROGROUP B:
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Citrone H., Clark E.B.,
RA Colton M.D., Ullendack T.R., Khouri H., Qin H., Vamathean J.,
RA Gill J., Scariato V., Maignani V., Plaza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappapoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58.";
RL Science 287:1809-1815(2000).
DR EMBL: AE002403; AAF40901.1; -.
DR HSSP: P00631; IQD5.
DR TIGR: NMB0464; -.
DR InterPro: IPR003187; PLA1.
DR Pfam: PF02253; PLA1; 1.
KW Complete proteome.
SQ SEQUENCE 382 AA; 42714 MW; B468A802F062B836 CRC64;
Query Match 2.0%; Score 9; DB 16; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 279 PEIPLTOPV 287
      |||||||
Db 221 PEIPLTOPV 229

RESULT 2
O9JT21 PRELIMINARY: PRT: 409 AA.
AC O9JT21:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Putative phospholipase.
GN NMA2021.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=655699;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
RA MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holtroyd S.,
RA Jørgensen K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis 22491."
RL Nature 404:502-506(2000).
DR EMBL: AL162757; CAB85240.1; -.
DR HSSP: P00631; 10D5.
DR InterPro: IPR003187; PLA1.
DR Pfam: PF02253; PLA1; 1.
KW Complete proteome.
SQ SEQUENCE 409 AA; 45862 MW; CD6585064D01A41 CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 16; Length 409;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 279 PEIPLTOPV 287
      |||||||
Db 248 PEIPLTOPV 256

RESULT 3
O9CL62 PRELIMINARY: PRT: 862 AA.
AC O9CL62:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE CysG.
GN CysG. OR PM1380.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RA MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida PM70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
REGULATORY COMPONENTS OF SENSOR TRANSDUCTION SYSTEMS.
CC -1- SIMILARITY: TO PROKARYOTE SENSOR TRANSDUCTION PROTEINS.
CC EMBL: AE006176; AAK03464.1; -.
DR InterPro: IPR003594; AtPbind_ArPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR003660; HAMP.
```

```
DR InterPro: IPR003661; His_kina.
DR InterPro: IPR004359; HIS_KIN_sig.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF006672; HAMP; 1.
DR Pfam: PF02518; HATPase_c; 1.
DR Pfam: PF00072; response_reg; 1.
DR Pfam: PF00512; signal; 1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR ProDom: PD000039; Response_reg; 1.
DR SMART: SM00304; HAMP; 1.
DR SMART: SM00387; HATPase_c; 1.
DR SMART: SM00388; HSKA; 1.
DR SMART: SM00448; REC; 1.
KW Kinase; Phosphorylation; Sensory transduction; Transferase;
KW Complete proteome.
SQ SEQUENCE 862 AA; 97846 MW; AB6814A3B63626C0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 16; Length 862;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LSTPLSTIL 13
      |||||||
Db 293 LSTPLSTIL 301

RESULT 4
O9AX85 PRELIMINARY: PRT: 1432 AA.
AC O9AX85:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Putative ABC transporter protein.
GN P0410E03.7.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriarthroideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone: P0410E03.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP002844; BAB21276.1; -.
DR InterPro: IPR003593; AAA_ArPase.
DR InterPro: IPR003439; ABC_transport.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC_transport; 1.
DR SMART: SM00382; AAA; 2.
KW ATP-binding.
SQ SEQUENCE 1432 AA; 160234 MW; 04E8CF2CA08D993 CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 10; Length 1432;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 170 FTPLSLFSD 178
      |||||||
Db 830 FTPLSLFSD 838

RESULT 5
O8TUS3 PRELIMINARY: PRT: 227 AA.
AC O8TUS3:
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Predicted phosphatase of the PHP family.
```

GN MK1681.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Stesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natsale D.A., Rogozin I.B., Ratusov R.L., Wolf Y.I., Stetter K.O.,
RA Mal'kh A.G., Kozin E.V., Kozavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL; AEO10457; AAM02894.1; -
KW Complete proteome.
SQ SEQUENCE 227 AA; 24975 MW; B80099EE2BA8912 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 17; Length 227;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 LVHGETPA 112
Db 106 LVHGETPA 113

RESULT 6

09M268
ID 09M268 PRELIMINARY; PRT; 299 AA.

AC 09M268;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE RAV-1like protein.
GN F21F14.140.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Choisene N., Robert C., Brotlier P., Wincker P., Catolico L.,
RA Attiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K.,
RA Mayer K.F.X., Queller F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL138642; CAB71904.1; -
DR InterPro: IPR003340; TF_B3.
DR Pfam: PF02362; B3; 1.
SQ SEQUENCE 299 AA; 34270 MW; 2AB841F179DD174B CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 10; Length 299;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 174 SLSPDLR 181
Db 292 SLSPDLR 299

RESULT 7

09CL22
ID 09CL22 PRELIMINARY; PRT; 306 AA.

AC 09CL22;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein PM1426.
GN PM1426.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70."
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AEO06179; AAK03510.1; -
DR HSSP; P00631; 10D6.
DR InterPro: IPR003187; PLAI.
DR Pfam: PF02253; PLAI; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 306 AA; 35580 MW; EAF3DE8C1C2B28E CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 16; Length 306;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 314 KLSRSMNR 321
Db 184 KLSRSMNR 191

RESULT 8

094ZC0
ID 094ZC0 PRELIMINARY; PRT; 415 AA.

AC 094ZC0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 2 (Fragment).
GN NAD2.
OS Isoetes duriei.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Lycopodiophyta; Isoetopsida; Isoetales; Isoetaceae; Isoetes.
OX NCBI_TaxID=56743;
RN [1]
RP SEQUENCE FROM N.A.
RA Knop V.;
RL "An extended molecular land plant phylogeny."
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AJ409119; CAC50076.1; -
DR InterPro: IPR001750; Oxidored_q1.
DR InterPro: IPR003880; Ppantne_attach.
DR Pfam: PF00361; Oxidored_q1; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 415 AA; 45082 MW; E0D3AC7820F6309 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 8; Length 415;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LSTLTLST 12
Db 341 LSTLTLST 348

RESULT 9

067608
ID 067608 PRELIMINARY; PRT; 55 AA.

AC 067608;

DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Tomato golden mosaic virus subgenomic DNA derived from DNA B ccdds -
 DE covalently closed circular double-stranded molecule.
 OS Tomato golden mosaic virus (TGMV).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10831;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87040767; PubMed=3022243;
 RA MacDowell S.W., Coutts R.H.A., Buck K.W.;
 RT "Molecular characterization of subgenomic single-stranded and double-
 RT stranded DNA forms isolated from plants infected with tomato golden
 RT mosaic virus.";
 RL Nucleic Acids Res. 14:7967-7984(1986).
 DR EMBL: X04485; CAA28171.1; -;
 DR InterPro: IPR000211; Gemin1_BL.
 DR Pfam: PF00845; Gemin1_BL; 1.
 SQ SEQUENCE 55 AA; 6281 MW; 41963570D739EC96 CRC64;

Query Match 1.6%; Score 7; DB 12; Length 55;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 SAKLSRS 318
 Db 43 SAKLSRS 49

RESULT 10
 Q92FV7 PRELIMINARY; PRT; 68 AA;
 AC Q92FV7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Hypothetical protein RC1370.
 GN RC1370.
 OS Rickettsia conorii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID=781;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MALISH 7;
 RX MEDLINE=21442074; PubMed=11557893;
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barde V.,
 RA Samson D., Roux V., Cossart P., Weissbach J., Claverie J.-M.,
 RA Raoult D.;
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
 RL Science 293:2093-2098(2001).
 DR EMBL: AE008682; AAL03908.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 68 AA; 7373 MW; 98F44F56AE4E8EC6 CRC64;

Query Match 1.6%; Score 7; DB 16; Length 68;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 TALENKT 84
 Db 45 TALENKT 51

RESULT 11
 Q91ZS4 PRELIMINARY; PRT; 72 AA.
 AC Q91ZS4;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Coat protein (Fragment).

GN CP.
 OS Potato virus Y strain NTN (PVY(NTN)).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OX NCBI_TaxID=122280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUBER NECROSING;
 RA Cerovska N., Filigarova M., Moravec T., Petrzik K.;
 RT "Differences in nucleotide and amino acid sequences of N-terminal
 RT parts of coat proteins among isolates of potato virus Y-NTN strain.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF228634; AAF67875.1; -;
 DR InterPro: IPR001592; Poty-coat.
 DR Pfam: PF00767; Poty-coat; 1.
 FT NON_TER 1 72
 FT NON_TER 1 72
 SQ SEQUENCE 72 AA; 7692 MW; 4F1298870523B482 CRC64;

Query Match 1.6%; Score 7; DB 12; Length 72;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 TKKDAQ 162
 Db 11 TKKDAQ 17

RESULT 12
 Q91ZS5 PRELIMINARY; PRT; 72 AA.
 AC Q91ZS5;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Coat protein (Fragment).
 GN CP.
 OS Potato virus Y strain NTN (PVY(NTN)).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OX NCBI_TaxID=122280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUBER NECROSING;
 RA Cerovska N., Filigarova M., Moravec T., Petrzik K.;
 RT "Differences in nucleotide and amino acid sequences of N-terminal
 RT parts of coat proteins among isolates of potato virus Y-NTN strain.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF228633; AAF67874.1; -;
 DR InterPro: IPR001592; Poty-coat.
 DR Pfam: PF00767; Poty-coat; 1.
 FT NON_TER 1 72
 FT NON_TER 1 72
 SQ SEQUENCE 72 AA; 7721 MW; 2C5287E15624CBDD CRC64;

Query Match 1.6%; Score 7; DB 12; Length 72;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 TKKDAQ 162
 Db 11 TKKDAQ 17

RESULT 13
 Q91ZS3 PRELIMINARY; PRT; 95 AA.
 AC Q91ZS3;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Coat protein (Fragment).
 GN CP.

```

OS   Potato virus Y strain NTN (PVY(NTN)).
OC   Viruses: ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC   Polyvirus.
OX   NCBI_TaxID=122280;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN-TUBER NECROSING;
RA   Czerovska N., Filigajova M., Moravec T., Petrzik K.;
RT   "Differences in nucleotide and amino acid sequences of N-terminal
RT   parts of coat proteins among isolates of potato virus Y-NTN strain.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR   EMBL: AF228635; AAF67876.1; -
DR   InterPro: IPR001592; Poly_coat.
DR   Pfam: PF00767; Poly_coat; 1.
FT   NON_TER 1
SQ   SEQUENCE 95 AA; 10446 MW; 28C06891777C9928 CRC64;

Query Match
Best Local Similarity 1.6%; Score 7; DB 12; Length 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 TKKDAQ 162
DB 11 TKKDAQ 17

RESULT 14
O91ZS8 PRELIMINARY; PRT; 96 AA.
AC O91ZS8:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Coat protein (Fragment).
GN CP.
OS Potato virus Y (strain N) (PVY).
OC Viruses: ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Polyvirus.
OX NCBI_TaxID=12219;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NECROSING;
RA Czerovska N., Filigajova M., Moravec T., Petrzik K.;
RT "Differences in nucleotide and amino acid sequences of N-terminal
RT parts of coat proteins among isolates of potato virus Y-NTN strain.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF228630; AAF67871.1; -
DR InterPro: IPR001592; Poly_coat.
DR Pfam: PF00767; Poly_coat; 1.
FT NON_TER 1
FT NON_TER 96
SQ SEQUENCE 96 AA; 10559 MW; 89C3A5675B9784CA CRC64;

Query Match
Best Local Similarity 1.6%; Score 7; DB 12; Length 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 TKKDAQ 162
DB 11 TKKDAQ 17

RESULT 15
O12148 PRELIMINARY; PRT; 100 AA.
AC O12148:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ORF YDL163W.
GN YDL163W.
OS Saccharomyces cerevisiae (Baker's yeast).

```

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OC   Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pohl T.M.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-ALPHAS288C;
RA Pohl T.M.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z74212; CAA98738.1; -
DR EMBL: Z67750; CAA91583.1; -
DR SGD: S0002322; YDL163W.
KW Hypothetical protein.
SQ SEQUENCE 100 AA; 10751 MW; 952FB92C852AA710 CRC64;

Query Match
Best Local Similarity 1.6%; Score 7; DB 3; Length 100;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LRLSILS 14
DB 26 LRLSILS 32

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Search completed: November 12, 2002, 11:48:21
Job time : 29.25 secs

11

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:40 ; Search time 30 Seconds
(without alignments)
1963.226 Million cell updates/sec

Title: US-09-787-083-4

Perfect score: 442
Sequence: 1 MKVSLSTLRLSLPCFAILA.....YNHEATSPFGVGLMLNDMGL 442

Scoring table:

OLIGO
Gapex 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	442	100.0	442	21	AAV85269 BASB034 amino acid
2	390	88.2	442	21	AAV85270 BASB034 amino acid
3	289	65.4	442	21	AAV85271 BASB034 amino acid
4	224	50.7	289	23	AAO17569 M catarrhalis MCAL
5	224	50.7	442	21	AAV85268 BASB034 amino acid
6	9	2.0	255	22	ABG18034 Novel human diagno
7	9	2.0	370	21	AAV75156 Neisseria gonorrhoe
8	9	2.0	370	21	AAV75157 Neisseria meningit
9	9	2.0	370	21	AAV75158 Neisseria meningit
10	9	2.0	374	21	AAV70629 Neisseria meningit

11	9	2.0	375	21	AAV70628 Neisseria meningit
12	8	1.8	278	21	AAG11137 Arabidopsis thalia
13	8	1.8	283	21	AAG11136 Arabidopsis thalia
14	8	1.8	299	21	AAG11135 Arabidopsis thalia
15	7	1.6	16	15	AAV82127 Mouse light chain
16	7	1.6	50	21	AAV79483 Rat alpha tubulin
17	7	1.6	64	21	AAV60322 Arabidopsis thalia
18	7	1.6	75	22	AAU22339 Human cardiovacu
19	7	1.6	82	21	AAV01488 Human secreted pro
20	7	1.6	99	22	AAU22308 Human cardiovacu
21	7	1.6	106	21	AAV07608 Arabidopsis thalia
22	7	1.6	106	21	AAV07608 Arabidopsis thalia
23	7	1.6	108	21	AAV37811 Arabidopsis thalia
24	7	1.6	114	22	AAU55952 Propionibacterium
25	7	1.6	116	21	AAV87313 Human signal pepti
26	7	1.6	116	23	ABG5204 Human albumin fusl
27	7	1.6	116	23	ABG5205 Human albumin fusl
28	7	1.6	116	23	ABG5206 Human secreted pro
29	7	1.6	116	23	AAU91093 Human secreted pro
30	7	1.6	116	23	AAU91120 Human secreted pro
31	7	1.6	116	23	AAU91121 Human secreted pro
32	7	1.6	133	22	ABG27556 Novel human diagno
33	7	1.6	136	21	AAV37810 Human ovarian anti
34	7	1.6	162	23	ABP42371 Chlamydia pneumoni
35	7	1.6	169	20	AAV34661 Arabidopsis thalia
36	7	1.6	181	21	AAV37809 Arabidopsis thalia
37	7	1.6	181	23	ABP42926 Human ovarian anti
38	7	1.6	186	21	AAV07607 Arabidopsis thalia
39	7	1.6	186	21	AAV51951 Arabidopsis thalia
40	7	1.6	190	21	AAV51950 Arabidopsis thalia
41	7	1.6	190	21	AAV07606 Arabidopsis thalia
42	7	1.6	221	23	ABG58103 Alfalfa mosaic vir
43	7	1.6	236	22	AAU55462 Human mdm2 protein
44	7	1.6	268	13	AAV21542 Envelope protein o
45	7	1.6	302	13	AAV24254 Protease inhibitor

ALIGNMENTS

RESULT 1
AAV85269 standard; Protein: 442 AA.

AC AAV85269;
XX
XX 29-JUN-2000 (first entry)
XX
XX BASB034 amino acid sequence #2.
DE
XX
XX Moraxella catarrhalis infection; BASB034; diagnosis; staging;
KW vaccine; bacteriostatic; treatment; prevention; otitis media; pneumonia;
KW sinusitis; nosocomial infection; invasive disease; chronic otitis media;
KW hearing loss; antibacterial drug.
XX
XX Moraxella catarrhalis.
OS
XX
XX WO200015802-A1.
PN
XX
XX 23-MAR-2000.
PD
XX
XX 14-SEP-1999; 99WO-EP06781.
PF
XX
XX 14-SEP-1998; 98GB-0020002.
PR
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX
XX Ruelle J;
XX
XX WPI: 2000-271440/23.
DR N-PSDB; AAA10701.
XX
XX Novel BASB034 polynucleotides and polypeptides from Moraxella

PT catarrhalis used to prepare vaccines against bacterial infections -
XX
XX Claim 3; Page 67; 106pp; English.
XX
CC This sequence represents a Moraxella catarrhalis BASB034 polypeptide from
CC strain Mc2908. The invention relates to BASB034 polypeptides from
CC M. catarrhalis strains Mc2931, Mc2908, Mc2913 and Mc2969. The BASB034
CC polynucleotides and polypeptides may be employed as research reagents and
CC material for the discovery of treatments and diagnostics for diseases,
CC particularly human diseases. They are particularly used to diagnose and
CC treat M. catarrhalis infections. They can be used for diagnosis of
CC disease, staging of disease, or determining response of an infectious
CC organism to drugs. The polynucleotides may be used as a source for
CC hybridization probes, and for screening of genetic mutations, serotype,
CC organism or strain identification, identification of mutations in BASB034
CC sequences, and as components of arrays which are useful for diagnostic
CC and prognostic purposes. The polypeptides can be used to produce
CC antibodies. The polypeptides can also be used in vaccine formulations,
CC and to identify agonists and antagonists. The polypeptides, antibodies,
CC agonists and antagonists (which are bacteriostatic) are used for the
CC treatment and prevention of diseases such as otitis media in infants and
CC children, pneumonia in elderlies, sinusitis, nosocomial infections and
CC invasive diseases, and chronic otitis media with hearing loss. The
CC polypeptides, agonists and antagonists are also used for screening of
CC antibacterial drugs. The BASB034 products of the invention can be used
CC screen for new antibacterial compounds that may target resistant
CC bacteria.
XX
XX Sequence 442 AA:
SQ
Query Match 100.0%; Score 442; DB 21; Length 442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKVSLSTLTSLTILPCFALIAIQAOAVNPVAFVDEYRSKNDLQDNDELLIGVOSATQSA 60
DB 1 MKVSLSTLTSLTILPCFALIAIQAOAVNPVAFVDEYRSKNDLQDNDELLIGVOSATQSA 60
QY 61 STDTANPLDEHEPELTYTALLENKTMKLINCSALNODIMRLACVDTLVHGERPAVITKRSI 120
DB 61 STDTANPLDEHEPELTYTALLENKTMKLINCSALNODIMRLACVDTLVHGERPAVITKRSI 120
QY 121 RLDETTIQTITKGRQVYVYQETTDPIFLMGNEKGMLTKKDAKOLEYAKQFTPLSLSDLD 180
DB 121 RLDETTIQTITKGRQVYVYQETTDPIFLMGNEKGMLTKKDAKOLEYAKQFTPLSLSDLD 180
QY 181 RNNTPLMSSRPNNPMYVLPITFMHGKPNRSPPTPSHEARQFTPNFRAPELKFOYSVAKA 240
DB 181 RNNTPLMSSRPNNPMYVLPITFMHGKPNRSPPTPSHEARQFTPNFRAPELKFOYSVAKA 240
QY 241 AEDLMGTDSDLMFGYTOOSHMQIFNGKNSRPFVHDYQPELFTQPYVSDLPMDGKVRMI 300
DB 241 AEDLMGTDSDLMFGYTOOSHMQIFNGKNSRPFVHDYQPELFTQPYVSDLPMDGKVRMI 300
QY 301 GMGAVHNSNGESAKLRSNMRAVYLMAGMEKNLTVMPRIMGRITKEGSGQPDNDPILD 360
DB 301 GMGAVHNSNGESAKLRSNMRAVYLMAGMEKNLTVMPRIMGRITKEGSGQPDNDPILD 360
QY 361 YGYGADVRFYQLEKNSNISGTVYRNPBSGKALQLDYVYPLGKISGYSFOIFOGYQSL 420
DB 361 YGYGADVRFYQLEKNSNISGTVYRNPBSGKALQLDYVYPLGKISGYSFOIFOGYQSL 420
QY 421 IDYHNEATSFYGVGLMLNDMMGL 442
DB 421 IDYHNEATSFYGVGLMLNDMMGL 442
RESULT 2
ID AAY85270 standard; Protein; 442 AA.
XX
XX AAY85270;
XX

DT 29-JUN-2000 (first entry)
XX
XX BASB034 amino acid sequence #3.
XX
KW Moraxella catarrhalis infection; BASB034; diagnosis; staging;
KW vaccine; bacteriostatic; treatment; prevention; otitis media; pneumonia;
KW sinusitis; nosocomial infection; invasive disease; chronic otitis media;
KW hearing loss; antibacterial drug.
XX
OS Moraxella catarrhalis.
XX
XX WO200015802-A1.
XX
XX 23-MAR-2000.
XX
PD 14-SEP-1999; 99WO-EP06781.
XX
PF 14-SEP-1998; 98GB-0020002.
XX
PR (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PA Ruelle J:
XX
PI WPI; 2000-271440/23.
XX
DR N-PSDB; AAA10702.
XX
DR Novel BASB034 polynucleotides and polypeptides from Moraxella
PT catarrhalis used to prepare vaccines against bacterial infections -
XX
XX Claim 3; Page 68; 106pp; English.
XX
XX
XX This sequence represents a Moraxella catarrhalis BASB034 polypeptide from
XX strain Mc2913. The invention relates to BASB034 polypeptides from
XX M. catarrhalis strains Mc2931, Mc2908, Mc2913 and Mc2969. The BASB034
XX polynucleotides and polypeptides may be employed as research reagents and
XX material for the discovery of treatments and diagnostics for diseases,
XX particularly human diseases. They are particularly used to diagnose and
XX treat M. catarrhalis infections. They can be used for diagnosis of
XX disease, staging of disease, or determining response of an infectious
XX organism to drugs. The polynucleotides may be used as a source for
XX hybridization probes, and for screening of genetic mutations, serotype,
XX organism or strain identification, identification of mutations in BASB034
XX sequences, and as components of arrays which are useful for diagnostic
XX and prognostic purposes. The polypeptides can be used to produce
XX antibodies. The polypeptides can also be used in vaccine formulations,
XX and to identify agonists and antagonists. The polypeptides, antibodies,
XX agonists and antagonists (which are bacteriostatic) are used for the
XX treatment and prevention of diseases such as otitis media in infants and
XX children, pneumonia in elderlies, sinusitis, nosocomial infections and
XX invasive diseases, and chronic otitis media with hearing loss. The
XX polypeptides, agonists and antagonists are also used for screening of
XX antibacterial drugs. The BASB034 products of the invention can be used
XX screen for new antibacterial compounds that may target resistant
XX bacteria.
XX
XX Sequence 442 AA:
SQ
Query Match 88.2%; Score 390; DB 21; Length 442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 53 VQSAQTQASTDTANPLDEHEPELTYTALLENKTMKLINCSALNODIMRLACVDTLVHGETPA 112
DB 53 VQSAQTQASTDTANPLDEHEPELTYTALLENKTMKLINCSALNODIMRLACVDTLVHGETPA 112
QY 113 VIKTKRSIRLDETTIQTITKGRQVYVYQETTDPIFLMGNEKGMLTKKDAKOLEYAKQFTP 172
DB 113 VIKTKRSIRLDETTIQTITKGRQVYVYQETTDPIFLMGNEKGMLTKKDAKOLEYAKQFTP 172
QY 173 LSLSFDDLRNNTPLMSSRPNNPMYVLPITFMHGKPNRSPPTPSHEARQFTPNFRAPELKF 232
DB 173 LSLSFDDLRNNTPLMSSRPNNPMYVLPITFMHGKPNRSPPTPSHEARQFTPNFRAPELKF 232

OY	233	OVSIVYKAAEDLWAGTDSIDLMPFGTQOSSHQIENFGKNSRPRVADYDQPEIFLTPPVSDLP	292
Db	233	VVVYKAAEDLWAGTDSIDLMPFGTQOSSHQIENFGKNSRPRVADYDQPEIFLTPPVSDLP	292
OY	293	WDGKVRMIGMGAHVHSHNSGESAKLRSRSMNRAIYLMAEGEMKLLTYMPRIWGRIFFEKSGSSQP	352
Db	293	WDGKVRMIGMGAHVHSHNSGESAKLRSRSMNRAIYLMAEGEMKLLTYMPRIWGRIFFEKSGSSQP	352
OY	353	DDNPDIIDYVYGVDVNFELYOLENKSNIISGTVRYNPPRSSGKALQLDVYVPLGKGISGYEQI	412
Db	353	DDNPDIIDYVYGVDVNFELYOLENKSNIISGTVRYNPPRSSGKALQLDVYVPLGKGISGYEQI	412
OY	413	FOGYGOSLIDYNNHEATSPFGVGLMLNPMKGL	442
Db	413	FOGYGOSLIDYNNHEATSPFGVGLMLNPMKGL	442
RESULT 3			
XX	AA85271	AA85271 standard; Protein; 442 AA.	
XX	AA85271;		
DT	29-JUN-2000	(first entry)	
XX			
DE	BASB034	amino acid sequence #4.	
XX			
KW	Moraxella catarrhalis infection; BASB034; diagnosis; staging;		
KW	vaccine; bacteriostatic; treatment; prevention; otitis media; pneumonia;		
KW	sinusitis; nosocomial infection; invasive disease; chronic otitis media;		
KW	hearing loss; antibacterial drug.		
XX			
OS	Moraxella catarrhalis.		
XX			
PN	MO200015802-A1.		
XX			
PD	23-MAR-2000.		
XX			
PF	14-SEP-1999; 99WO-EP06781.		
XX			
PR	14-SEP-1998; 98GB-0020002.		
XX			
PA	(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.		
XX			
PI	Ruelle J;		
XX			
DR	WPI: 2000-271440/23.		
XX			
DR	N-PSDB; AAA10703.		
XX			
PT	Novel BASB034 polynucleotides and polypeptides from Moraxella		
PT	catarrhalis used to prepare vaccines against bacterial infections		
XX			
PS	Claim 3; Page 69; 106pp; English.		
XX			
CC	This sequence represents a Moraxella catarrhalis BASB034 polypeptide from		
CC	strain Mc2969. The invention relates to BASB034 polypeptides from		
CC	M. catarrhalis strains Mc2931, Mc2908, Mc2913 and Mc2969. The BASB034		
CC	polynucleotides and polypeptides may be employed as research reagents and		
CC	material for the discovery of treatments and diagnostics for diseases,		
CC	particularly human diseases. They are particularly used to diagnose and		
CC	treat M. catarrhalis infections. They can be used for diagnosis of		
CC	disease, staging of disease, or determining response of an infectious		
CC	organism to drugs. The polynucleotides may be used as a source for		
CC	hybridization probes, and for screening of genetic mutations, serotype,		
CC	organism or strain identification. Identification of mutations in BASB034		
CC	sequences, and as components of arrays which are useful for diagnostic		
CC	and prognostic purposes. The polypeptides can be used to produce		
CC	antibodies. The polypeptides can also be used in vaccine formulations,		
CC	and to identify agonists and antagonists. The polypeptides, antibodies,		
CC	agonists and antagonists (which are bacteriostatic) are used for the		
CC	treatment and prevention of diseases such as otitis media in infants and		
CC	children, pneumonia in elderly, sinusitis, nosocomial infections and		
CC	invasive diseases, and chronic otitis media with hearing loss. The		

CC	polypeptides; agonists and antagonists are also used for screening of
CC	antibacterial drugs. The BABS034 products of the invention can be used
CC	screen for new antibacterial compounds that may target resistant
CC	bacteria.
xx	
SQ	Sequence 442 AA;
	Query Match 65.4%; Score 289; DB 21; Length 442;
	Best Local Similarity 99.7%; Pred. No. 5,9e-773;
	Matches 389; Conservative 0; Mismatches 1; Indels 0; Gaps
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DB	53 VQSATQSASTPTAPLDEHEPELYTTALEKKTMLINCSALNODIMRLACTDPLVHGEPFA 112
OY	VLTKRISRLEDETLMOTIKGPGVVYOETDPILFMGNENEGMILTKKDAOLEYAAKOFTF 172
DB	113 VLTKRISRLEDETLMOTIKGPGVVYOETDPILFMGNENEGMILTKKDAOLEYAAKOFTF 172
OY	LLSFLSDLRRNTPLWSSRPHPNPVLPILFHNGKPNNSPNTPSHEAKOFTPNFEPAELKF 232
DB	173 LLSFLSDLRRNTPLWSSRPHPNPVLPILFHNGKPNNSPNTPSHEAKOFTPNFEPAELKF 232
OY	QVSVKVKAEDLMCTDDSLMFNGYQOSHMOIFMGKKSRRPRVNDXOPELFITLOPYSDLP 292
DB	233 QVSVKVKAEDLMCTDDSLMFNGYQOSHMOIFMGKKSRRPRVNDXOPELFITLOPYSDLP 292
OY	WDGKVRMIGMCAVHNSNGESAKLSRSNNRAYLMAGMEMKKLVMPRIIMGRIKEGSGSQP 352
DB	293 WDGKVRMIGMCAVHNSNGESAKLSRSNNRAYLMAGMEMKKLVMPRIIMGRIKEGSGSQP 352
OY	DNDPDILDYVGVDREFLYOLENKSNISGTVRYNPRSFGALQLDYVPYLGGKISGYFOI 412
DB	353 DNDPDILDYVGVDREFLYOLENKSNISGTVRYNPRSFGALQLDYVPYLGGKISGYFOI 412
OY	FQGIGOSLIDYNHEATSFYGGLINDMAGL 442
DB	413 FQGIGOSLIDYNHEATSFYGGLINDMAGL 442
RESULT 4	
AAOI17569	
ID	AAOI17569 standard; Protein; 289 AA.
XX	
AC	AAOI17569;
XX	
DT	19-JUL-2002 (first entry)
XX	
DE	M catarrhalis MCA100712 protein SEQ ID NO: 18.
XX	
KW	Moraxella; vaccine; respiratory tract infection; antiinflammatory;
XX	auditory; antibacterial; otitis media; sinusitis; pneumonia.
OS	Moraxella catarrhalis.
XX	
PM	WO200218595-A2.
PD	07-MAR-2002.
XX	
PF	28-AUG-2001; 2001WO-CA01221.
XX	
PR	28-AUG-2000; 2000US-228294P.
PR	28-AUG-2000; 2000US-228295P.
PR	28-AUG-2000; 2000US-228296P.
PR	29-AUG-2000; 2000US-228438P.
PR	29-AUG-2000; 2000US-228439P.
PR	29-AUG-2000; 2000US-228440P.
PR	29-AUG-2000; 2000US-228441P.
PR	29-AUG-2000; 2000US-228442P.
PR	29-AUG-2000; 2000US-228443P.
PR	29-AUG-2000; 2000US-228511P.
PR	29-AUG-2000; 2000US-228512P.
PR	29-AUG-2000; 2000US-228742P.

PR 29-AUG-2000; 2000US-228773P.
 PR 01-SEP-2000; 2000US-229465P.
 PR 01-SEP-2000; 2000US-229474P.
 PR 01-SEP-2000; 2000US-229475P.
 PR 01-SEP-2000; 2000US-229478P.
 PR 05-SEP-2000; 2000US-229740P.
 PR 05-SEP-2000; 2000US-229803P.
 PR 05-SEP-2000; 2000US-229804P.
 PR 05-SEP-2000; 2000US-229805P.
 PR 05-SEP-2000; 2000US-229806P.
 PR 05-SEP-2000; 2000US-229809P.
 PR 05-SEP-2000; 2000US-229811P.
 PR 06-SEP-2000; 2000US-230214P.
 PR 06-SEP-2000; 2000US-230250P.
 PR 06-SEP-2000; 2000US-230252P.
 XX
 PA (AVER) AVENTIS PASTEUR LTD.
 PT Loomore S, Wang J, Bradley B, Ochs M, Yang Y;
 PI WPI; 2002-401721/43.
 DR N-PSDB; AAL46501.
 XX
 PT Moraxella polypeptide and polynucleotides useful as vaccine for
 immunizing a host e.g. humans against disease e.g. otitis media,
 pneumonia, caused by infection of the bacteria
 PT pneumonia, caused by infection of the bacteria
 PS Claim 28; Fig 17; 277pp; English.
 XX
 CC The present invention provides the protein and coding sequences of
 CC proteins from Moraxella catarrhalis. These can be used to produce
 CC vaccines which protect against M. catarrhalis infection, which can cause
 CC otitis media, respiratory infection, sinusitis, and pneumonia. The
 CC present sequence is a protein of the invention.
 CC
 XX
 SQ Sequence 289 AA:
 Query Match 50.7%; Score 224; DB 23; Length 289;
 Best Local Similarity 100.0%; Pred. No. 9.2e-210;
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 219 QFTPNFRAPRLKFOVSVKKAEDLWGTDSDLMFGYTOOSHMOIFNGKNSRPRVHDYQ 278
 DB 66 QFTPNFRAPRLKFOVSVKKAEDLWGTDSDLMFGYTOOSHMOIFNGKNSRPRVHDYQ 125
 QY 279 PEIFLTQPVYSDLPWDGKVRMIGMAVHNSGESAKLSRSNMNRAVYLMAGHEMKNLTVMPR 338
 DB 126 PEIFLTQPVYSDLPWDGKVRMIGMAVHNSGESAKLSRSNMNRAVYLMAGHEMKNLTVMPR 185
 QY 339 IMGRIFKEGSGSQPDNDPDLIDYGYDVRFLYOLEKNSNIGTVRNPNRSGKALOLDY 398
 DB 186 IMGRIFKEGSGSQPDNDPDLIDYGYDVRFLYOLEKNSNIGTVRNPNRSGKALOLDY 245
 QY 399 VYPLGKGISGYFOIFOGYOSLIDYNEHATSFVGLMLNDMMGL 442
 DB 246 VYPLGKGISGYFOIFOGYOSLIDYNEHATSFVGLMLNDMMGL 289
 RESULT 5
 AAY85268
 ID AAY85268 standard; Protein: 442 AA.
 AC AAY85268;
 XX
 DT 29-JUN-2000 (first entry)
 XX
 DE BASB034 amino acid sequence #1.
 XX
 KW Moraxella catarrhalis infection; BASB034; diagnosis; staging;
 KW vaccine; bacteriostatic; treatment; prevention; otitis media; pneumonia;
 KW sinusitis; nosocomial infection; invasive disease; chronic otitis media;
 KW hearing loss; antibacterial drug.
 XX

OS Moraxella catarrhalis.
 XX
 PN WC200015802-A1.
 XX
 PD 23-MAR-2000.
 XX
 PF 14-SEP-1999; 99WO-EP06781.
 XX
 PR 14-SEP-1998; 98GB-0020002.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Ruelle J;
 XX
 DR WPI; 2000-271440/23.
 DR N-PSDB; AAA10700.
 XX
 PT Novel BASB034 polynucleotides and polypeptides from Moraxella
 PT catarrhalis used to prepare vaccines against bacterial infections
 PT
 PS Claim 3; Fig 2; 106pp; English.
 XX
 CC This sequence represents a Moraxella catarrhalis BASB034 polypeptide from
 CC strain Mc2931 (ATCC 43617). The invention relates to BASB034 polypeptides
 CC from M. catarrhalis strains Mc2931, Mc2908, Mc2913 and Mc2969. The
 CC BASB034 polynucleotides and polypeptides may be employed as research
 CC reagents and material for the discovery of treatments and diagnostics for
 CC diseases, particularly human diseases. They are particularly used to
 CC diagnose and treat M. catarrhalis infections. They can be used for
 CC diagnosis of disease, staging of disease, or determining response of an
 CC infectious organism to drugs. The polynucleotides may be used as a source
 CC for hybridization probes, and for screening of genetic mutations,
 CC serotype, organism or strain identification, identification of mutations
 CC in BASB034 sequences, and as components of arrays which are useful for
 CC diagnostic and prognostic purposes. The polypeptides can be used to
 CC produce antibodies. The polypeptides can also be used in vaccine
 CC formulations, and to identify agonists and antagonists. The polypeptides,
 CC antibodies, agonists and antagonists (which are bacteriostatic) are used
 CC for the treatment and prevention of diseases such as otitis media in
 CC infants and children, pneumonia in elderly, sinusitis, nosocomial
 CC infections and invasive diseases, and chronic otitis media with hearing
 CC loss. The polypeptides, agonists and antagonists are also used for
 CC screening of antibacterial drugs. The BASB034 products of the invention
 CC can be used screen for new antibacterial compounds that may target
 CC resistant bacteria.
 CC
 XX
 SQ Sequence 442 AA:
 Query Match 50.7%; Score 224; DB 21; Length 442;
 Best Local Similarity 100.0%; Pred. No. 1.3e-209;
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 219 QFTPNFRAPRLKFOVSVKKAEDLWGTDSDLMFGYTOOSHMOIFNGKNSRPRVHDYQ 278
 DB 219 QFTPNFRAPRLKFOVSVKKAEDLWGTDSDLMFGYTOOSHMOIFNGKNSRPRVHDYQ 278
 QY 279 PEIFLTQPVYSDLPWDGKVRMIGMAVHNSGESAKLSRSNMNRAVYLMAGHEMKNLTVMPR 338
 DB 279 PEIFLTQPVYSDLPWDGKVRMIGMAVHNSGESAKLSRSNMNRAVYLMAGHEMKNLTVMPR 338
 QY 339 IMGRIFKEGSGSQPDNDPDLIDYGYDVRFLYOLEKNSNIGTVRNPNRSGKALOLDY 398
 DB 339 IMGRIFKEGSGSQPDNDPDLIDYGYDVRFLYOLEKNSNIGTVRNPNRSGKALOLDY 398
 QY 399 VYPLGKGISGYFOIFOGYOSLIDYNEHATSFVGLMLNDMMGL 442
 DB 399 VYPLGKGISGYFOIFOGYOSLIDYNEHATSFVGLMLNDMMGL 442
 RESULT 6
 ABG18034
 ID ABG18034 standard; Protein: 255 AA.
 XX

AC ABG18034;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #18025.
 XX
 KM Human: chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001: 2001WO-US08631.
 XX
 PR 31-MAR-2000: 2000US-0540217.
 PR 23-AUG-2000: 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS62221.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20: SEQ ID No 48393; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SO Sequence 255 AA;
 XX
 Query Match 2.0%; Score 9; DB 22; Length 255;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 279 PEIFLTQPV 287
 DB 204 PEIFLTQPV 212
 IIIIIIIIII
 RESULT 7
 AA75156
 ID AAY75156 standard; Protein; 370 AA.
 AC AAY75156;
 XX

DT 21-MAR-2000 (first entry)
 XX
 DE Neisseria gonorrhoeae ORF 582 protein sequence SEQ ID NO:1786.
 XX
 KM Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 XX antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
 KM antibacterial; gene therapy.
 XX
 OS Neisseria gonorrhoeae.
 XX
 PN WO957280-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-US09346.
 XX
 PR 01-MAY-1998; 98US-0083758.
 PR 31-JUL-1998; 98US-0094869.
 PR 02-SEP-1998; 98US-0098994.
 PR 02-SEP-1998; 98US-0099062.
 PR 09-OCT-1998; 98US-0103749.
 PR 09-OCT-1998; 98US-0103794.
 PR 09-OCT-1998; 98US-0103796.
 PR 25-FEB-1999; 99US-0121528.
 XX
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;
 PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
 PI Tettelin H, Venter JC;
 XX
 DR WPI: 2000-062150/05.
 DR N-PSDB; AA253918.
 XX
 PT Novel Neisserial polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics -
 XX
 PS Claim 2; Page 903; 1453pp; English.
 XX
 CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
 CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of
 CC the invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the
 CC manufacture of medicaments for treating or preventing infection due to
 CC Neisserial bacteria (e.g. meningitis and septicemia), to detect the
 CC presence of Neisseria bacteria, or to raise antibodies. They may also
 CC be used to screen for agonists or antagonists, which may themselves
 CC have use as antibacterial agents. The polynucleotides of the invention
 CC may also be used in gene therapy protocols.
 XX
 SO Sequence 370 AA;
 XX
 Query Match 2.0%; Score 9; DB 21; Length 370;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 279 PEIFLTQPV 287
 DB 209 PEIFLTQPV 217
 IIIIIIIIII
 RESULT 8
 AA75157
 ID AAY75157 standard; Protein; 370 AA.
 AC AAY75157;
 XX
 DT 21-MAR-2000 (first entry)
 XX

DE Neisseria meningitidis ORF 582 protein sequence SEQ ID NO:1788.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KW antibacterial; gene therapy.
XX
OS Neisseria meningitidis.
XX
PN WO957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI: 2000-062150/05.
DR N-PSDB: AA253919.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics -
XX
PS Claim 2; Page 904; 1453pp; English.
XX
CC AA253015 to AA254536, AA254577 to AA254615, and AA774253 to AA775941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC Neisserial bacteria (e.g. meningitis and septicaemia), to detect the
CC presence of Neisseria bacteria, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
XX
SQ Sequence 370 AA:
Query Match 2.0%; Score 9; DB 21; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 279 PEIPLTQPV 287
DB 209 PEIPLTQPV 217
RESULT 9
AA75158
ID AA75158 standard; Protein; 370 AA.
XX
AC AA75158;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 582 protein sequence SEQ ID NO:1790.
XX

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KW antibacterial; gene therapy.
XX
OS Neisseria meningitidis.
XX
PN WO957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI: 2000-062150/05.
DR N-PSDB: AA253920.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics -
XX
PS Claim 2; Page 905; 1453pp; English.
XX
CC AA253015 to AA254536, AA254577 to AA254615, and AA774253 to AA775941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC Neisserial bacteria (e.g. meningitis and septicaemia), to detect the
CC presence of Neisseria bacteria, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
XX
SQ Sequence 370 AA:
Query Match 2.0%; Score 9; DB 21; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 279 PEIPLTQPV 287
DB 209 PEIPLTQPV 217
RESULT 10
AA70629
ID AA70629 standard; Protein; 374 AA.
XX
AC AA70629;
XX
DT 18-JUL-2000 (first entry)
XX
DE Neisseria meningitidis serogroup B strain H44/76 BASB033 protein.
XX
KW BASB033; diagnosis; prophylaxis; treatment; antibacterial; vaccine;
KW Neisseria meningitidis infection.

XX OS Neisseria meningitidis.
XX PN WO200015801-A1.
XX PD 23-MAR-2000.
XX PF 09-SEP-1999; 99WO-EP06718.
XX PR 14-SEP-1998; 98GB-0020003.
XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Ruelle J;
XX DR WPI; 2000-271439/23.
XX DR N-PSDB; AA252134.
XX PT Isolated BASB033 polypeptides and polynucleotides of Neisseria
XX PT meningitidis, useful for diagnosis, prophylaxis and treatment of N.
XX PT meningitidis infection -
XX PS Claim 4; Page 59; 93pp; English.
XX CC The present sequence is a BASB033 protein from
CC Neisseria meningitidis serogroup B strain H44/76. The protein
CC shows homology to the Klebsiella pneumoniae outer membrane
CC phospholipase A. The present sequence is useful for diagnosis,
CC prophylaxis and treatment of N. meningitidis infection. It may also be
CC used for the discovery and development of antibacterial compounds and
CC in vaccine compositions.
SQ Sequence 374 AA;
QY Query Match 2.0%; Score 9; DB 21; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 279 PEIPLTOPV 287
IIIIIIIIII
DB 213 PEIPLTOPV 221

RESULT 11
ID AAY70628 standard; Protein; 375 AA.
XX AAY70628;
XX AC AAY70628;
XX DT 18-JUL-2000 (first entry)
XX DE Neisseria meningitidis serogroup B strain ATCC13090 BASB033 protein.
XX KM BASB033; diagnosis; prophylaxis; treatment; antibacterial; vaccine;
KM Neisseria meningitidis infection.
XX OS Neisseria meningitidis.
XX PN WO200015801-A1.
XX PD 23-MAR-2000.
XX PF 09-SEP-1999; 99WO-EP06718.
XX PR 14-SEP-1998; 98GB-0020003.
XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Ruelle J;
XX DR WPI; 2000-271439/23.
XX DR N-PSDB; AA252133.
XX

PT Isolated BASB033 polypeptides and polynucleotides of Neisseria
PT meningitidis, useful for diagnosis, prophylaxis and treatment of N.
PT meningitidis infection -
XX PS Claim 4; Page 58; 93pp; English.
XX CC The present sequence is a BASB033 protein from
CC Neisseria meningitidis serogroup B strain ATCC13090. The protein
CC shows homology to the Klebsiella pneumoniae outer membrane
CC phospholipase A. The present sequence is useful for diagnosis,
CC prophylaxis and treatment of N. meningitidis infection. It may also be
CC used for the discovery and development of antibacterial compounds and
CC in vaccine compositions.
SQ Sequence 375 AA;
QY Query Match 2.0%; Score 9; DB 21; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 279 PEIPLTOPV 287
IIIIIIIIII
DB 214 PEIPLTOPV 222

RESULT 12
ID AAG11137 standard; Protein; 278 AA.
XX AAG11137;
XX AC AAG11137;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 9741.
XX KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX XX 25-FEB-2000; 2000EP-0301439.
XX PF 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
XX PR 29-MAR-1999; 99US-0126785.
XX PR 01-APR-1999; 99US-0127462.
XX PR 06-APR-1999; 99US-0128234.
XX PR 08-APR-1999; 99US-0128714.
XX PR 16-APR-1999; 99US-0129845.
XX PR 19-APR-1999; 99US-0130077.
XX PR 21-APR-1999; 99US-0130449.
XX PR 23-APR-1999; 99US-0130510.
XX PR 28-APR-1999; 99US-0130891.
XX PR 30-APR-1999; 99US-0131449.
XX PR 30-APR-1999; 99US-0132048.
XX PR 04-MAY-1999; 99US-0132407.
XX PR 05-MAY-1999; 99US-0132484.
XX PR 06-MAY-1999; 99US-0132485.
XX PR 06-MAY-1999; 99US-0132486.
XX PR 07-MAY-1999; 99US-0132487.
XX PR 11-MAY-1999; 99US-0134256.
XX PR 14-MAY-1999; 99US-0134218.
XX PR 14-MAY-1999; 99US-0134219.
XX PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139819.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142977.
PR 12-JUL-1999; 99US-0143462.
PR 13-JUL-1999; 99US-0143624.
PR 14-JUL-1999; 99US-0144005.
PR 15-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
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PR 27-JUL-1999; 99US-0145513.

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PR 03-AUG-1999; 99US-0147038.
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PR 23-AUG-1999; 99US-0149930.
PR 23-AUG-1999; 99US-0149930.
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PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151303.
PR 01-SEP-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154019.
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PR 20-SEP-1999; 99US-0154779.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 25-OCT-1999; 99US-0161405.

PR 25-OCT-1999; 99US-0161406.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 1.8%; Score 8; DB 21; Length 278;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 174 SLSEFLDR 181
Db 271 SLSEFLDR 278

RESULT 13
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ID AG1136 standard; Protein; 283 AA.
XX
AC AG1136;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9740.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hydrolisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128274.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
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PR 27-MAY-1999; 99US-0136392.
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PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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PR 23-JUL-1999; 99US-0145218.
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PR 28-JUL-1999; 99US-0145951.
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PR 03-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.
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PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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PR 11-AUG-1999; 99US-0148319.
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PR 13-AUG-1999; 99US-0148664.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0150930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
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PR 24-SEP-1999; 99US-0156559.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
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PR 28-OCT-1999; 99US-0161970.
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PR 28-OCT-1999; 99US-0161993.
PR 28-OCT-1999; 99US-0161993.

PR 29-OCT-1999; 99US-0162142.
Query Match 1.8%; Score 8; DB 21; Length 283;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 174 SLSEFIDLR 181
Db 276 SLSEFIDLR 283
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ID AAG1135 standard; Protein: 299 AA.
XX
AC AAG1135;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9739.
XX
KW Protein identification: signal transduction pathway; metabolic pathway;
KW hydrolisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123348.
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PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
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PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.

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PR 26-JUL-1999; 99US-0145276.
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PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 03-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.

PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
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PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 26-OCT-1999; 99US-0161361.
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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 1.8%; Score 8; DB 21; Length 299;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 174 SLSFDR 181

Db 292 SLSEDLDR 299

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RESULT 15

AA52127
ID AAR52127 standard; peptide: 16 AA.

AC AAR52127;

DT 27-SEP-1996 (first entry)

DE Mouse light chain surface patch S03410.

XX antibody; humanised; murine; human; heavy chain; light; variable;
KW framework region; complementarity determining region; reshaping;
KW modelling; surface residue; modify.

OS Mus sp.

PN EP592106-A1.

PD 13-APR-1994.

PF 07-SEP-1993; 93EP-0307051.

PR 09-SEP-1992; 92US-0942245.

PA (PEDE/) PEDERSEN J T.
(IMMU-) IMMUNOGEN INC.

PI Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;

DR WPI: 1994-120230/15.

PT Method of resurfacing of rodent antibodies to produce humanised
PT antibody forms - for producing non-human antibodies with improved
PT therapeutic efficiency by presenting human surface on V-region

PS Example 1; Page 14; 230pp; English.

XX Modification of a rodent antibody or fragment by resurfacing in order
CC to produce a humanised rodent antibody can be determined by calculating
CC homology between murine and human antibody surfaces. In order to test
CC the resurfacing approach of the invention, three humanisation
CC experiments were set up. (1) traditional loop grafting; (2) resurfacing
CC approach using most similar chain; and (3) resurfacing approach using
CC human sequences with most similar surface residues. AAR52069-159 are the
CC surface residue patterns in mouse light chain antibody variable regions.
CC These "patches" were used in the third method, where rodent light and
CC heavy chains were matched and the most similar human sequence found
CC independently only over the surface residues indicated in AAR52030-67.

SQ Sequence 16 AA;

Query Match 1.6%; Score 7; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 25;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 387 PRSGKA 393

DB 4 PRSGKA 10

Search completed: November 12, 2002, 11:44:51
Job time : 31 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:46 ; Search time 11 Seconds
(Without alignments)
1182.267 Million cell updates/sec

Title: US-09-787-083-4

Perfect score: 442
Sequence: 1 MKVSLSTLTSLTSLPCFAILA.....YNHEATSFYGLMLNDWGL 442

Scoring table: OLIGO

Gapex 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size: 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCrus.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	1.6	16	1	US-07-942-245-98
2	7	1.6	552	1	US-08-231-729B-6
3	7	1.6	900	4	US-08-890-865A-4
4	7	1.6	934	1	US-08-215-805A-80
5	7	1.6	1026	2	US-08-542-003-6
6	7	1.6	1026	2	US-08-322-760A-6
7	7	1.6	1026	4	US-09-236-949-6
8	6	1.4	10	3	US-08-974-775-30
9	6	1.4	11	3	US-08-974-775-29
10	6	1.4	12	3	US-08-974-775-28
11	6	1.4	13	3	US-08-974-775-8
12	6	1.4	13	3	US-08-974-775-27
13	6	1.4	14	3	US-08-974-775-9
14	6	1.4	14	3	US-08-974-775-10
15	6	1.4	14	3	US-08-974-775-32
16	6	1.4	15	3	US-08-974-775-5
17	6	1.4	16	3	US-08-974-775-4
18	6	1.4	20	1	US-08-430-273-1
19	6	1.4	21	1	US-07-918-953-13
20	6	1.4	21	1	US-07-918-953-15
21	6	1.4	21	1	US-08-212-696-1
22	6	1.4	21	1	US-08-158-245-1
23	6	1.4	21	1	US-08-081-661-13
24	6	1.4	21	1	US-08-081-661-15
25	6	1.4	21	1	US-08-233-617-1
26	6	1.4	21	1	US-08-160-376A-1
27	6	1.4	21	1	US-08-304-070-1

28	6	1.4	21	1	US-08-285-661-1	Sequence 1, Appli
29	6	1.4	21	1	US-08-301-838-1	Sequence 1, Appli
30	6	1.4	21	1	US-08-389-487-4	Sequence 4, Appli
31	6	1.4	21	1	US-08-389-487-12	Sequence 12, Appli
32	6	1.4	21	1	US-08-507-124-2	Sequence 2, Appli
33	6	1.4	21	1	US-08-507-124-3	Sequence 3, Appli
34	6	1.4	21	1	US-08-342-931-1	Sequence 1, Appli
35	6	1.4	21	1	US-08-400-286-1	Sequence 1, Appli
36	6	1.4	21	2	US-08-508-664-9	Sequence 9, Appli
37	6	1.4	21	2	US-08-353-476-85	Sequence 85, Appli
38	6	1.4	21	2	US-08-353-476-87	Sequence 87, Appli
39	6	1.4	21	2	US-08-484-219-1	Sequence 1, Appli
40	6	1.4	21	2	US-08-979-587-1	Sequence 1, Appli
41	6	1.4	21	2	US-08-992-676-1	Sequence 1, Appli
42	6	1.4	21	2	US-08-992-676-6	Sequence 6, Appli
43	6	1.4	21	2	US-09-134-836-1	Sequence 1, Appli
44	6	1.4	21	2	US-09-134-836-7	Sequence 7, Appli
45	6	1.4	21	3	US-08-967-867-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-07-942-245-98
Sequence 98, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GOLLID, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngene, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-33202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-98

Query Match 1.6%, Score 7, DB 1, Length 16;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 387 PRSGKA 393
|||||
Db 4 PRSGKA 10

RESULT 2
US-08-231-729B-6
; Sequence 6, Application US/08231729B
; Patent No. 5618722
; GENERAL INFORMATION:
; APPLICANT: ZENNO, Shubel
; APPLICANT: SHIRAIISHI, Shinji
; APPLICANT: INOUE, Satoshi
; APPLICANT: SAIGO, Kaeiru
; TITLE OF INVENTION: FIREFLY LUCIFERASE GENE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEYDIG, VOIT & MAYER
; STREET: 700 Thirteenth Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,729B
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 119050/1993
; FILING DATE: 21-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rose, Herbert C.
; REGISTRATION NUMBER: 29846
; REFERENCE/DOCKET NUMBER: 60130/No. 5618722aKa
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-737-6770
; TELEFAX: 202-737-6776
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 552 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-231-729B-6
Query Match 1.6%; Score 7; DB 1; Length 552;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 175 LSPDLR 181
Db 184 LSPDLR 190
RESULT 3
US-08-890-865A-4
; Sequence 4, Application US/08890865A
; Patent No. 6307019
; GENERAL INFORMATION:
; APPLICANT: Constantini, Franklin
; APPLICANT: Zeng, Li
; TITLE OF INVENTION: AXIN GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,865A
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/54249
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-890-865A-4
Query Match 1.6%; Score 7; DB 4; Length 900;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 403 GKGISGY 409
Db 268 GKGISGY 274
RESULT 4
US-08-215-805A-80
; Sequence 80, Application US/08215805A
; Patent No. 5559008
; GENERAL INFORMATION:
; APPLICANT: Chang, Yung-Fu
; TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURILLA
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/215,805A
; FILING DATE: 22-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 934 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Pasteurella suis
; STRAIN: 5943

IMMEDIATE SOURCE:
LIBRARY: P. suis DNA in Bacteriophage lambda-dash
CLONE: (lambda)Yfc33-37
US-08-215-805A-80

Query Match 1.6%; Score 7; DB 1; Length 934;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 238 VKAEDL 244
|||||
Db 62 VKAEDL 68

RESULT 5
US-08-542-003-6
Sequence 6, Application US/08542003
Patent No. 5864013
GENERAL INFORMATION:
APPLICANT: Goldberg, Edward B.
TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF
TITLE OF INVENTION: NANOMETER STRUCTURES AND USE THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542.003
FILING DATE: 13-OCT-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION/DOCKET NUMBER: 18,872
TELEPHONE: (212) 790-9090
TELEFAX: 212-869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacteriophage T4
IMMEDIATE SOURCE:
CLONE: p37 amino acid
US-08-542-003-6

Query Match 1.6%; Score 7; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 QTIRKP 134
|||||
Db 861 QTIRKP 867

RESULT 6
US-08-322-760A-6
Sequence 6, Application US/08322760A
Patent No. 5877279
GENERAL INFORMATION:

APPLICANT: Goldberg, Edward B.
TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF
TITLE OF INVENTION: NANOMETER STRUCTURES AND USE THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322.760A
FILING DATE: 13-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION/DOCKET NUMBER: 18,872
TELEPHONE: (212) 790-9090
TELEFAX: 212-869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacteriophage T4
IMMEDIATE SOURCE:
CLONE: p37 amino acid
US-08-322-760A-6

Query Match 1.6%; Score 7; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 QTIRKP 134
|||||
Db 861 QTIRKP 867

RESULT 7
US-09-236-949-6
Sequence 6, Application US/09236949
Patent No. 6437112
GENERAL INFORMATION:
APPLICANT: Goldberg, Edward B.
TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF
TITLE OF INVENTION: NANOMETER STRUCTURES AND USE THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236.949
FILING DATE: 25-Jan-1999

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/542,003
; FILING DATE: 13-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: 212-869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1026 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacteriophage T4
; IMMEDIATE SOURCE:
; CLONE: p37 amino acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-236-949-6
Query Match 1.6%; Score 7; DB 4; Length 1026;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 128 QTIKGP 134
DB 861 QTIKGP 867
RESULT 8
US-08-974-775-30
; Sequence 30, Application US/08974775
; Patent No. 6096706
; GENERAL INFORMATION:
; APPLICANT: Toback, F. Gary
; APPLICANT: Walsh-Reltz, Margaret
; TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
; TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
; STREET: NBC Tower - Suite 3600, 455 N. Cityfront
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60611-5599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,775
; FILING DATE: 20-NOV-1997
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin, Alice O.
; REGISTRATION NUMBER: 35,601
; REFERENCE/DOCKET NUMBER: 7814/27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-321-4200
; TELEFAX: 312-321-4299
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-775-30
Query Match 1.4%; Score 6; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 424 NHEATS 429
DB 5 NHEATS 10
RESULT 9
US-08-974-775-29
; Sequence 29, Application US/08974775
; Patent No. 6096706
; GENERAL INFORMATION:
; APPLICANT: Toback, F. Gary
; APPLICANT: Walsh-Reltz, Margaret
; TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
; TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
; STREET: NBC Tower - Suite 3600, 455 N. Cityfront
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60611-5599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,775
; FILING DATE: 20-NOV-1997
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin, Alice O.
; REGISTRATION NUMBER: 35,601
; REFERENCE/DOCKET NUMBER: 7814/27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-321-4200
; TELEFAX: 312-321-4299
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-775-29
Query Match 1.4%; Score 6; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 424 NHEATS 429
DB 5 NHEATS 10
RESULT 10
US-08-974-775-28
; Sequence 28, Application US/08974775
; Patent No. 6096706
; GENERAL INFORMATION:
; APPLICANT: Toback, F. Gary
; APPLICANT: Walsh-Reltz, Margaret
; TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
```


TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-28

Query Match 1.4%; Score 6; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
|||||
Db 5 NHEATS 10

RESULT 11
US-08-974-775-8
Sequence 8, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.

REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-8

Query Match 1.4%; Score 6; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
|||||
Db 8 NHEATS 13

RESULT 12
US-08-974-775-27
Sequence 27, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-27

Query Match 1.4%; Score 6; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
|||||
Db 5 NHEATS 10

RESULT 13
US-08-974-775-9
Sequence 9, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
APPLICANT: Walsh-Reitz, Margaret
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-9
Query Match 1.4%; Score 6; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 424 NHEATS 429
DB 8 NHEATS 13

RESULT 14
US-08-974-775-10
Sequence 10, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
APPLICANT: Walsh-Reitz, Margaret
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-974-775-10
Query Match 1.4%; Score 6; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 424 NHEATS 429
DB 8 NHEATS 13

RESULT 15
US-08-974-775-32
Sequence 32, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
APPLICANT: Walsh-Reitz, Margaret
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: /product= "Ser or Tyr"
US-08-974-775-32

Query Match 1.4%; Score 6; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 424 NHEATS 429
|||||
Db 8 NHEATS 13

Search completed: November 12, 2002, 11:49:12
Job time : 12 secs

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; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PAM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1082
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (45)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (90)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-764-869-1082
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Query Match 1.6%; Score 7; DB 10; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 34 VDEVRK 40
DB 67 VDEVRK 73
```

```
RESULT 3
US-09-773-882-2
; Sequence 2, Application US/09773882
; Patent No. US20020106769A1
; GENERAL INFORMATION:
; APPLICANT: Omura, Mitsuo
; APPLICANT: Inagaki, Tomoko
; APPLICANT: Matsumoto, Ryoji
; APPLICANT: Moriguchi, Takaya
; APPLICANT: Hasegawa, Shin
; APPLICANT: Suhayda, Charles
; TITLE OF INVENTION: UDP-D-Glucose:Limonoid Glucosyltransferase
; FILE REFERENCE: 0119.98
; CURRENT APPLICATION NUMBER: US/09/773,882
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-021179
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Citrus unshiu
US-09-773-882-2
```

```
Query Match 1.6%; Score 7; DB 10; Length 511;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 32 AFVDEVR 38
DB 459 AFVDEVR 465
```

```
RESULT 4
US-09-773-882-11
; Sequence 11, Application US/09773882
; Patent No. US20020106769A1
; GENERAL INFORMATION:
; APPLICANT: Omura, Mitsuo
; APPLICANT: Inagaki, Tomoko
; APPLICANT: Matsumoto, Ryoji
```

```
; APPLICANT: Moriguchi, Takaya
; APPLICANT: Hasegawa, Shin
; APPLICANT: Suhayda, Charles
; TITLE OF INVENTION: UDP-D-Glucose:Limonoid Glucosyltransferase
; FILE REFERENCE: 0119.98
; CURRENT APPLICATION NUMBER: US/09/773,882
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-021179
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Citrus unshiu
US-09-773-882-11
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```
Query Match 1.6%; Score 7; DB 10; Length 511;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 32 AFVDEVR 38
DB 459 AFVDEVR 465
```

```
RESULT 5
US-09-815-242-11029
; Sequence 11029, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haseibeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes In
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 11029
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-11029
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```
Query Match 1.6%; Score 7; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 168 KOTPLS 174
DB 434 KOTPLS 440
```

RESULT 6

US-09-825-144-2
; Sequence 2, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Matthias Krause
; APPLICANT: Antonio S. Sechl
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Wehland
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 783
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-144-2

Query Match

Best Local Similarity 1.6%; Score 7; DB 10; Length 783;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 268 NSRPFV 274
|||||

Db 17 NSRPFV 23

RESULT 7

US-09-825-144-4
; Sequence 4, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Matthias Krause
; APPLICANT: Antonio S. Sechl
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Wehland
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-144-4

Query Match

Best Local Similarity 1.6%; Score 7; DB 10; Length 829;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 268 NSRPFV 274
|||||

Db 17 NSRPFV 23

RESULT 8

US-09-947-770-20
; Sequence 20, Application US/09947770
; Patent No. US20020068715A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Ruiz, Pedro

; APPLICANT: Garren, Hideki

; TITLE OF INVENTION: DNA Vaccination for Treatment of

; TITLE OF INVENTION: Autoimmune Disease

; FILE REFERENCE: STAN123CIP

; CURRENT APPLICATION NUMBER: US/09/947,770

; CURRENT FILING DATE: 2001-09-05

; PRIOR APPLICATION NUMBER: PCT/US00/06233

; PRIOR FILING DATE: 2000-03-10

; PRIOR APPLICATION NUMBER: US 09/267,590

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Insulin A (7-21) peptide

US-09-947-770-20

Query Match

Best Local Similarity 1.4%; Score 6; DB 10; Length 15;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 LYOLEN 375
|||||

Db 7 LYOLEN 12

RESULT 9

US-09-732-561-23
; Sequence 23, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
; APPLICANT: Thomma, Bart
; APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
; APPLICANT: Manners, John
; APPLICANT: Kazan, Kemal
; APPLICANT: Brockaert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Ag Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/202,638
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/01672
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: PPD 50165/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-732-561-23

Query Match 1.4%; Score 6; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 GYGQSL 420
|||||
DB 11 GYGQSL 16

RESULT 10
US-09-947-563-1
; Sequence 1, Application US/09947563
; Patent No. US20020156234A1
; GENERAL INFORMATION:
; APPLICANT: Rudroder, Franz-Josef
; Kellner, Reinhold

TITLE OF INVENTION: Improved process for obtaining
insulin precursors having correctly bonded cystine bridges

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/947,563

FILING DATE: 07-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/134,836

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Leslie McDowell

REGISTRATION NUMBER: 34,872

REFERENCE/DOCKET NUMBER: 02481.1600-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Escherichia coli

FEATURE:

NAME/KEY: Protein

LOCATION: 1..21

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-947-563-1

Query Match 1.4%; Score 6; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 LYOLEN 375
|||||

DB 13 LYOLEN 18

RESULT 11
US-09-947-563-7
; Sequence 7, Application US/09947563
; Patent No. US20020156234A1
; GENERAL INFORMATION:

APPLICANT: Rudroder, Franz-Josef
Kellner, Reinhold

TITLE OF INVENTION: Improved process for obtaining
insulin precursors having correctly bonded cystine bridges

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/947,563

FILING DATE: 07-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/134,836

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Leslie McDowell

REGISTRATION NUMBER: 34,872

REFERENCE/DOCKET NUMBER: 02481.1600-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Escherichia coli

FEATURE:

NAME/KEY: Protein

LOCATION: 1..21

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-947-563-7

Query Match 1.4%; Score 6; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 LYOLEN 375
|||||
DB 13 LYOLEN 18

RESULT 12
US-09-853-844-1
; Sequence 1, Application US/09853844
; Patent No. US2002013269A1
; GENERAL INFORMATION:

APPLICANT: Balschmidt, Per
Brange, Vellgaard Jens Jorgen

TITLE OF INVENTION: Human Insulin Analogues
FILE REFERENCE: 3343.270-US

;; CURRENT APPLICATION NUMBER: US/09/853,844
;; CURRENT FILING DATE: 2001-05-11
;; PRIOR APPLICATION NUMBER: 08/965,221
;; PRIOR FILING DATE: 1997-11-06
;; PRIOR APPLICATION NUMBER: 08/531,842
;; PRIOR FILING DATE: 1995-09-21
;; PRIOR APPLICATION NUMBER: 08/275,196
;; PRIOR FILING DATE: 1994-07-14
;; PRIOR APPLICATION NUMBER: 07/976,805
;; PRIOR FILING DATE: 1992-11-16
;; PRIOR APPLICATION NUMBER: 07/453,445
;; PRIOR FILING DATE: 1989-12-20
;; PRIOR APPLICATION NUMBER: 07/416,218
;; PRIOR FILING DATE: 1989-10-02
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-853-844-1

Query Match 1.4%; Score 6; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 LYOLEN 375
Db 13 LYOLEN 18

RESULT 13
US-09-815-229-1
;; Sequence 1, Application US/09815229
;; Patent No. US200200586141
;; GENERAL INFORMATION:
;; APPLICANT: Filvaroff, Ellen H.
;; APPLICANT: Okumu, Franklin W.
;; TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGEOUS DISORDERS
;; FILE REFERENCE: P1786RIUS
;; CURRENT APPLICATION NUMBER: US/09/815,229
;; CURRENT FILING DATE: 2001-03-22
;; PRIOR APPLICATION NUMBER: US 60/192,103
;; PRIOR FILING DATE: 2000-03-24
;; NUMBER OF SEQ ID NOS: 17
;; SEQ ID NO 1
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-815-229-1

Query Match 1.4%; Score 6; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 LYOLEN 375
Db 13 LYOLEN 18

RESULT 14
US-10-066-151-102
;; Sequence 102, Application US/10066151
;; Patent No. US20020132300A1
;; GENERAL INFORMATION:
;; APPLICANT: Hogan, Patrick G.
;; APPLICANT: Rao, Anjana
;; APPLICANT: Aramburu, Jose
;; TITLE OF INVENTION: SPECIFIC INHIBITORS OF NFAT ACTIVATION
;; TITLE OF INVENTION: BY CALCINEURIN AND THEIR USE IN TREATING IMMUNE-RELATED
;; FILE REFERENCE: 10861-004002
;; CURRENT APPLICATION NUMBER: US/10/066,151

;; CURRENT FILING DATE: 2002-01-31
;; PRIOR APPLICATION NUMBER: 09/248,620
;; PRIOR FILING DATE: 1999-02-11
;; PRIOR APPLICATION NUMBER: 60/074,467
;; PRIOR FILING DATE: 1998-02-12
;; NUMBER OF SEQ ID NOS: 114
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 102
;; LENGTH: 22
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetically generated peptide containing the
;; OTHER INFORMATION: SPRIETPS amino acid sequence
US-10-066-151-102

Query Match 1.4%; Score 6; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 TPSHEA 217
Db 15 TPSHEA 20

RESULT 15
US-09-864-761-43426
;; Sequence 43426, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wenshang
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;; FILE REFERENCE: Aeomica-x-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43426
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031587.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
US-09-864-761-43426

Query Match 1.4%; Score 6; DB 10; Length 26;
Best Local Similarly 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 KEGGS 350
|11111|
DB 9 KEGGS 14

Search completed: November 12, 2002, 11:49:41
Job time : 7.75 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:45 ; Search time 13.75 Seconds
(without alignments)
3090.285 Million cell updates/sec

Title: US-09-787-083-4

Perfect score: 442

Sequence: 1 MKVSLSTLTLSTLPCFALLA.....YVHEATSEGVGLMDNMGL 442

Scoring table: OLIGO

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2.0	382	2	E81195	phospholipase A1,
2	2.0	409	2	H81831	probable phospholip
3	1.8	286	2	B36971	outer membrane pho
4	1.8	299	2	T47989	RAV-like protein -
5	1.8	1396	2	S36851	L-shaped tail fibre
6	1.6	68	2	B97871	hypothetical prote
7	1.6	112	2	C97787	hypothetical prote
8	1.6	122	2	E75377	hypothetical prote
9	1.6	155	2	A29699	beta-lactoglobulin
10	1.6	158	2	E86498	Pts IIA Protein [I
11	1.6	158	2	E72124	pts IIA protein -
12	1.6	164	2	E97061	integrase xerD fam
13	1.6	194	2	C95982	probable membrane
14	1.6	197	2	A54506	tubulin alpha-1 ch
15	1.6	219	2	T19438	hypothetical prote
16	1.6	233	2	AD3344	hypothetical prote
17	1.6	240	2	A61544	tubulin alpha chai
18	1.6	264	2	A44959	coat protein - pot
19	1.6	267	2	A60366	coat protein - pot
20	1.6	267	2	S14001	genome polypote
21	1.6	267	2	S26630	capsid protein - p
22	1.6	267	2	JC1527	coat protein - p
23	1.6	267	2	S13339	tail fiber protein
24	1.6	270	2	S73734	abc transport ATP-
25	1.6	273	2	C72328	transaminase B hom
26	1.6	288	2	T36237	probable phosphor
27	1.6	292	2	E72576	probable ABC trans
28	1.6	306	2	T27985	hypothetical prote
29	1.6	307	2	B87659	hydrolase, probabl

30	7	1.6	310	2	T02200	probable RAV-like
31	7	1.6	313	2	U70960	polyprotein - pota
32	7	1.6	324	2	T23876	hypothetical prote
33	7	1.6	326	2	A43939	proteinase inhibit
34	7	1.6	338	2	F69437	hypothetical prote
35	7	1.6	342	2	G64411	hypothetical prote
36	7	1.6	342	2	C64394	hypothetical prote
37	7	1.6	343	2	AG2465	hypothetical prote
38	7	1.6	349	2	T43920	yfuc protein (impo
39	7	1.6	349	2	G90400	ubiquinol-cytochro
40	7	1.6	357	2	A45619	probable dihydroli
41	7	1.6	370	2	G83219	genome polyprotein
42	7	1.6	379	2	S13556	ribonuclease D VCI
43	7	1.6	381	2	G82132	tail fiber protein
44	7	1.6	382	2	S13237	tubulin alpha chai
45	7	1.6	384	2	S70638	

ALIGNMENTS

RESULT 1
E81195
phospholipase A1, probable NMB0464 [imported] - Neisseria meningitidis (strain MC58 s
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: E81195
R:Retelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignanl, V.; Pizzu, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappoia, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: AB1000; M0ID:2015755; PMID:10710307
A:Accession: E81195
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1382 <RET>
A:Cross-references: GB:AE002403; GB:AE002096; NID:g7225688; PIDN:AAF40901.1; PID:g722
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0464

Query Match 2.0%; Score 9; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 279 PEIFLRQPV 287
|||||||
Db 221 PEIFLRQPV 229

RESULT 2
H81831
probable phospholipase NMA2021 [imported] - Neisseria meningitidis (strain Z2491 serog
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: H81831
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: AB1775; M0ID:20222556; PMID:10761919
A:Accession: H81831
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1409 <PAR>
A:Cross-references: GB:AL62757; GB:AL157959; NID:g7380371; PIDN:CAB85240.1; PID:g738
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA2021

Query Match 2.0%; Score 9; DB 2; Length 409;

Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 279 PEIFLTOPY 287
|||||||
DB 248 PEIFLTOPY 256

RESULT 3

B36971
outer membrane phospholipase A (EC 3.1.1.-) precursor - Klebsiella pneumoniae
C:Species: Klebsiella pneumoniae
C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 18-Jun-1999
C:Accession: B36971; S40129
R:Brook, R.G.P.M.; Brinkman, E.; van Boxtel, R.; Bekkers, A.C.A.P.A.; Verheij, H.M.; Tomm
J. Bacteriol. 176, 861-870, 1994
A:Title: Molecular characterization of enterobacterial plid genes encoding outer membra
A:Reference number: A36971; MUID:94131966; PMID:8300539
A:Accession: B36971
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <BRO>
A:Cross-references: EMBL:X76901; NID:g436880; PIDN:CAA54223.1; PID:g436881
A:Note: authors translated the codon AAG for residue 112 as Arg
C:Genetics:
A:Gene: plidA
C:Superfamily: bacterial phospholipase A1
C:Keywords: carboxylic ester hydrolase

Query Match 1.8%; Score 8; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 431 GVGMLMD 438
|||||||
DB 277 GVGMLMD 284

RESULT 4

T47989
RAV-1-like protein - Arabidopsis thaliana
N:Alternate names: protein F21F14.140
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47989
R:Chism, N.; Robert, C.; Brotlier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Se
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24481
A:Accession: T47989
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <CHO>
A:Cross-references: EMBL:AL138642
A:Experimental source: cultivar Columbia; BAC clone F21F14
C:Genetics:
A:Map position: 3
A:Note: F21F14.140

Query Match 1.8%; Score 8; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 174 SLSEFLDR 181
|||||||
DB 292 SLSEFLDR 299

RESULT 5

S36851
L-shaped tail fiber protein - phage T5
N:Alternate names: ltf protein
C:Species: phage T5
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000

C:Accession: S65934; S01984; S36851
R:Kallman, A.V.; Kulshin, V.E.; Shlyapnikov, M.G.; Ksenzenko, V.N.; Kryukov, V.M.
FEBS Lett. 366, 46-48, 1995
A:Title: The nucleotide sequence of the bacteriophage T5 ltf gene.
A:Reference number: S65934; MUID:95309401; PMID:7789514
A:Accession: S65934
A:Molecule type: DNA

A:Residues: 1-1396 <KAL>
A:Cross-references: EMBL:X69460; NID:g15415; PIDN:CAA49220.1; PID:g15416
R:Kallman, A.V.; Kryukov, V.M.; Bayev, A.A.
Nucleic Acids Res. 16, 6230, 1988
A:Title: The nucleotide sequence of bacteriophage T5 DNA at the region between early
A:Reference number: S01984; MUID:88289370; PMID:3267228
A:Accession: S01984
A:Status: translation not shown

A:Molecule type: DNA
A:Residues: 934-985, 'A', 987-1396 <KA2>
A:Cross-references: EMBL:X07559
C:Genetics:
A:Gene: ltf
C:Keywords: late protein; tail fiber

Query Match 1.8%; Score 8; DB 2; Length 1396;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 OSATQSAS 61
|||||||
DB 87 OSATQSAS 94

RESULT 6

B97871
hypothetical protein RC1370 [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C:Accession: B97871
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: B97871
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <KUR>
A:Cross-references: GB:AE006914; PIDN:AAL03908.1; PID:g15620515; GSPDB:GN00173
C:Genetics:
A:Gene: RC1370

Query Match 1.6%; Score 7; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 TALENKT 84
|||||||
DB 45 TALENKT 51

RESULT 7

C97787
hypothetical protein RC0699 [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C:Accession: C97787
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: C97787
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-112 <KUR>
A:Cross-references: GB:AE006914; PIDN:AAL03237.1; PID:g15619790; GSPDB:GN00173

C:Genetics:
A:Gene: RC0699

Query Match 1.6%; Score 7; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NDGQDN 47
DB 85 NDGQDN 91

RESULT 8
E75377
hypothetical protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: E75377
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75377
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-122 <WHI>
A:Cross-references: GB:AE002002; GB:AE00513; NID:96459345; PIDN:AAFI1150.1; PID:9645935
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1580
A:Map position: 1

Query Match 1.6%; Score 7; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 EHEPELY 76
DB 115 EHEPELY 121

RESULT 9
A29699
beta-lactoglobulin - eastern gray kangaroo
C:Species: *Macropus giganteus* (eastern gray kangaroo)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jul-1997
C:Accession: A29699
R:Godoyac-Zimmermann, J.; Shaw, D.
Biol. Chem. Hoppe-Seyler 368, 879-886, 1987
A:Title: The primary structure, binding site and possible function of beta-lactoglobulin
A:Reference number: A29699; MUID:87299024; PMID:3620116
A:Accession: A29699
A:Molecule type: protein
A:Residues: 1-155 <GOD>
C:Superfamily: lipocalin; lipocalin homology
F:10-155/Domain: lipocalin homology <LIP>

Query Match 1.6%; Score 7; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 RSKNDLG 44
DB 5 RSKNDLG 11

RESULT 10
E86498
Pta IIA Protein (Imported) - *Chlamydomonas reinhardtii* (strain J138)
C:Species: *Chlamydomonas reinhardtii*
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: E86498
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of *Chlamydomonas reinhardtii* J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: E86498
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <STO>
A:Cross-references: GB:BA000008; NID:98978434; PIDN:BA098271.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: ptn1
C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannitol

Query Match 1.6%; Score 7; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSTLTLS 11
DB 126 LSTLTLS 132

RESULT 11
E72124
Pta IIA protein - *Chlamydomonas reinhardtii* (strain CML029)
C:Species: *Chlamydomonas reinhardtii*
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C:Accession: E72124
R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of *Chlamydomonas reinhardtii* and *C. trachomatis*.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: E72124
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <ARN>
A:Cross-references: GB:AE001591; GB:AE001363; NID:94376311; PIDN:AMD18213.1; PID:9437
A:Experimental source: strain CML029
C:Genetics:
A:Gene: ptn1
C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannitol
F:28-156/Domain: phosphotransferase system mannitol-specific enzyme II factor III hom

Query Match 1.6%; Score 7; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSTLTLS 11
DB 126 LSTLTLS 132

RESULT 12
E97061
Integrase XerD family protein (similarity only with C-terminal part) [Imported] - *Clostridium acetobutylicum*
C:Species: *Clostridium acetobutylicum*
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: E97061
R:Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome sequence and comparative analysis of the solvent-producing bacterium
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97061
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-164 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK79280.1; PID:915024240; GSPDB:GN00168
A:Experimental source: *Clostridium acetobutylicum* ATCC824
C:Genetics:
A:Gene: CAC1310

Query Match 1.6%; Score 7; DB 2; Length 164;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 QLENKSN 378
 |||||||
 DB 49 QLENKSN 55

RESULT 13

C95982
 probable membrane protein, similar to periplasmic nitrate reductase Nntr [Imported] - S.
 C:Species: *Sinorhizobium meliloti*
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: C95982
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98: 9889-9894, 2001
 A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: C95982
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-194 <KUR>
 A:Cross-references: GB:AL591985; PIDN:CAC49523.1; PID:g15141010; GSPDB:GN00167
 A:Experimental source: strain 1021, megaplasmid pSymb
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaul, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welis, D.H.; Wong, K.; Yen, K.
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: Smb20997
 A:Genome: plasmid

Query Match 1.6%; Score 7; DB 2; Length 194;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ELLIGVQ 54
 |||||||
 DB 184 ELLIGVQ 190

RESULT 14

A54506
 tubulin alpha-1 chain - Plasmodium yoelii (fragment)
 C:Species: *Plasmodium yoelii*
 C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 13-Aug-1999
 C:Accession: A54506
 R:Arkella, R.; Arasu, P.; Valdyra, A.B.
 Mol. Biochem. Parasitol. 30, 165-174, 1988
 A:Title: Molecular clones of alpha-tubulin genes of *Plasmodium yoelii* reveal an unusual
 A:Reference number: A54506; MUID:89014607; PMID:2459618
 A:Accession: A54506
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-197 <AKES>
 A:Cross-references: GB:M29816; NID:g160729; PIDN:AAA29779.1; PID:g160730
 C:Superfamily: tubulin

Query Match 1.6%; Score 7; DB 2; Length 197;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 IKTKRSI 120
 |||||||
 DB 82 IKTKRSI 88

RESULT 15

T19438
 hypothetical protein C25A1.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T19438
 R:Mortimore, B.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19124
 A:Accession: T19438
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-219 <NIL>
 A:Cross-references: EMBL:Z81038; PIDN:CAB02762.1; GSPDB:GN00019; CESP:C25A1.1
 C:Experimental source: clone C25A1
 C:Genetics:
 A:Gene: CESP:C25A1.1
 A:Map position: 1
 A:Introns: 33/1; 66/1; 151/2

Query Match 1.6%; Score 7; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 KDAKQLE 164
 |||||||
 DB 52 KDAKQLE 58

Search completed: November 12, 2002, 11:46:30
 Job time : 15.75 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:45 ; Search time 7.5 Seconds

(without alignments)
2444.338 Million cell updates/sec

Title: US-09-787-083-4

Perfect score: 442
Sequence: 1 MKVSLSTLTLSTLPCFALLA.....YHNEATSPGVGLMNDMGL 442

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	1.8	286	1	PAL_KLEPN
2	8	1.8	1396	1	PLF_BPT5
3	7	1.6	155	1	LACH_MACGI
4	7	1.6	174	1	LACH_MACEU
5	7	1.6	197	1	TBA_PLAYO
6	7	1.6	212	1	PRL_ICIPU
7	7	1.6	240	1	TBA_OCTPU
8	7	1.6	270	1	Y304_MYCPN
9	7	1.6	273	1	ILVE_THEMA
10	7	1.6	322	1	MIAA_PSEPU
11	7	1.6	326	1	SPL_BACBR
12	7	1.6	342	1	FLAD_METJA
13	7	1.6	342	1	Y755_METJA
14	7	1.6	423	1	AMT_AOUAE
15	7	1.6	444	1	TBA_ONCKE
16	7	1.6	448	1	TBA_HUMAN
17	7	1.6	448	1	TBA5_CHICK
18	7	1.6	449	1	TBAE_DROME
19	7	1.6	449	1	TBAE_PHYPO
20	7	1.6	449	1	TBAN_PHYPO
21	7	1.6	449	1	TBA_XENLA
22	7	1.6	450	1	TBAD_PHYPO
23	7	1.6	450	1	TBA_PHYPO
24	7	1.6	450	1	TBA_HAECO
25	7	1.6	451	1	TBA1_NORVI
26	7	1.6	451	1	TBA1_HUMAN
27	7	1.6	451	1	TBA_OCTDO
28	7	1.6	451	1	TBA_TORMA
29	7	1.6	511	1	LGT_CITUN
30	7	1.6	513	1	ATPA_HAEIN
31	7	1.6	536	1	60IM_BUCAP
32	7	1.6	544	1	GPI0_DICDI
33	7	1.6	567	1	GPV_RAT

34	7	1.6	610	1	FIMB_DICDI	P54680 dictyostel1
35	7	1.6	635	1	DNAM_HALMA	001100 halobacula
36	7	1.6	681	1	CAO2_HUMAN	099424 homo sapien
37	7	1.6	768	1	YB23_HUMAN	094177 homo sapien
38	7	1.6	783	1	FYB_HUMAN	015117 homo sapien
39	7	1.6	862	1	AXN1_HUMAN	015169 homo sapien
40	7	1.6	862	1	LKTA_PASSP	P55123 pasteurella
41	7	1.6	947	1	VG37_BPT4	P03744 bacteriopho
42	7	1.6	1026	1	POLG_PYTBU	002963 p genome po
43	7	1.6	3061	1	POLG_PYTBU	P40838 rana esculi
44	6	1.4	33	1	BR2B_RANES	P32423 rana esculi
45	6	1.4	50	1	YK05_CABEL	P34300 caenorhabdi

ALIGNMENTS

RESULT 1	PAL_KLEPN	STANDARD;	PRT;	286 AA.
ID	PAL_KLEPN			
AC	P37446;			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	01-OCT-1994 (Rel. 30, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	Phospholipase A1 precursor (EC 3.1.1.32) (Detergent-resistant			
DE	phospholipase A) (DR-phospholipase A) (Phosphatidylcholine 1-			
DE	acylhydrolase) (Outer membrane phospholipase A) (OM PLA).			
GN	PLA.			
OS	Klebsiella pneumoniae.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OX	Klebsiella.			
OX	NCBI_TaxID=573;			
RN	[1]			
RX	SEQUENCE FROM N.A.			
RA	MEDLINE=94131966; PubMed=8300539;			
RA	Brok R.G.P.M., Brinkman E., van Bortel R., Bekkers A.C.A.P.,			
RA	Verheij H.M., Tomassen J.;			
RT	"Molecular characterization of enterobacterial plid genes encoding			
RT	outer membrane phospholipase A."			
RL	J. Bacteriol. 176:861-870(1994).			
CC	- FUNCTION: HYDROLYSIS OF PHOSPHATIDYLCHOLINE WITH PHOSPHOLIPASE			
CC	A2 (EC 3.1.1.4) AND PHOSPHOLIPASE A1 (EC 3.1.1.32) ACTIVITIES.			
CC	- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-			
CC	acylglycerophosphocholine + a fatty acid anion.			
CC	- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 2-			
CC	acylglycerophosphocholine + a fatty acid anion.			
CC	- COFACTOR: REQUIRES CALCIUM IONS FOR ACTIVITY.			
CC	- SUBCELLULAR LOCATION: OUTER MEMBRANE; ONE OF THE VERY FEW ENZYMES			
CC	LOCATED THERE.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL: X76901; CAA54223.1; -			
DR	PIR: B36971; B36971.			
DR	PIR: S40129; S40129.			
DR	HSSP: P00631; 10D6.			
DR	InterPro: IPR003187; PLA1.			
DR	Pfam: PF02253; PLA1; 1.			
KW	PRINTS: PR01486; PPHPLIPASEA1.			
KW	Hydrolase; Lipid degradation; Outer membrane; Signal; Calcium.			
FT	SIGNAL	1	286	BY SIMILARITY.
FT	CHAIN	21	286	BY SIMILARITY.
FT	ACT_SITE	161	161	BY SIMILARITY.
FT	SEQUENCE	286 AA;	32544 MW;	3E39F865085108A3 CRC64;
Query Match	1.88;	Score 8;	DB 1;	Length 286;
Best Local Similarity	100.0%;	Pred. No. 1.6;		

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 GVGILMND 438
 |||||
 Db 277 GVGILMND 284

RESULT 2
 ID VITE_BPT5 STANDARD; PRT; 1396 AA.
 AC P13390; O48502;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE L-shaped tail fiber protein (LTF protein).
 GN LTF.
 OS Bacteriophage T5.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC T5-like viruses.
 OX NCBI_TaxID=10726;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95309401; PubMed=7789514;
 RA Kallman A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.,
 RA Kryukov V.M.;
 RT "The nucleotide sequence of the bacteriophage T5 ltf gene.";
 RL FEBS Lett. 366:46-48(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Kallman A.V.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE=88289370; PubMed=3267228;
 RA Kallman A.V., Kryukov V.M., Bayev A.A.;
 RT "The nucleotide sequence of bacteriophage T5 DNA at the region
 between early and late genes.";
 RL Nucleic Acids Res. 16:6230-6230(1988).
 CC -1- FUNCTION: NONESSENTIAL PROTEIN THAT MEDIATES BINDING TO THE
 CC POLYMANNOSE O ANTIGEN.
 CC -----
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 CC -----
 CC EMBL: X69460; CAA49220.1; -;
 DR EMBL; AJ001191; CAA04591.1; -;
 DR PIR; S01982; S01982.
 KM Late protein.
 FT CONFLICT 986 986 V -> A (IN REF. 2).
 SQ SEQUENCE 1396 AA; 147989 MW; 18CD2192F65FEFFC1 CRC64;

Query Match 1.8%; Score 8; DB 1; Length 1396;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QSATQSAS 61
 |||||
 Db 87 QSATQSAS 94

RESULT 3
 LACB_MACGI STANDARD; PRT; 155 AA.
 ID LACB_MACGI
 AC P11944;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Beta-lactoglobulin.

GN LCB.
 OS Macropus giganteus (Eastern gray kangaroo).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=9317;
 RN (1)
 RP SEQUENCE
 RX MEDLINE=87299024; PubMed=3620116;
 RA Godovac-Zimmermann J., Shaw D.;
 RT "Beta-lactoglobulin identified in marsupial milk. The primary
 RT structure, binding site and possible function of beta-lactoglobulin
 RT from eastern grey kangaroo (Macropus giganteus).";
 RL Biol. Chem. Hoppe-Seyler 368:879-886(1987).
 CC -1- FUNCTION: LACTOGLOBULIN IS THE PRIMARY COMPONENT OF WHEY, IT
 CC BINDS RETINOL AND IS PROBABLY INVOLVED IN THE TRANSPORT OF
 CC THAT MOLECULE.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY.
 CC PIR; A29699; A29699.
 DR HSSP; P02754; 1BSQ.
 DR InterPro; IPR000566; Lipocln-cytfabp.
 DR Pfam; PF00061; Lipocalin_1.
 DR PROSITE; PS00213; LIPOCALIN; FALSE NEG.
 KW Milk; Whey; Retinol-binding; Transport; Lipocalin.
 FT DISULFID 61 153 BY SIMILARITY.
 FT DISULFID 103 115 BY SIMILARITY.
 SQ SEQUENCE 155 AA; 18340 MW; 7BD7E4A191530E5 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 155;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 RSKNDLG 44
 |||||
 Db 5 RSKNDLG 11

RESULT 4
 LACB_MACEU STANDARD; PRT; 174 AA.
 ID LACB_MACEU
 AC Q29614;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Beta-lactoglobulin precursor.
 GN LCB OR B1G.
 OS Macropus eugenii (Tamar wallaby).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=9315;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91197370; PubMed=1707629;
 RA Collet C., Joseph R., Nicholas K.R.;
 RT "A marsupial beta-lactoglobulin gene: characterization and prolactin-
 RT dependent expression.";
 RL J. Mol. Endocrinol. 6:9-16(1991).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95314595; PubMed=7794241;
 RA Collet C., Joseph R.;
 RT "Exon organization and sequence of the genes encoding alpha-
 RT lactalbumin and beta-lactoglobulin from the tamar wallaby
 RT (Macropodidae, Marsupialia).";
 RL Biochem. Genet. 33:61-72(1995).
 RN (3)
 RP SEQUENCE OF 47-174 FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=95085593; PubMed=7993373;
 RA Collet C., Joseph R.;
 RT "The identification of nuclear and mitochondrial genes by sequencing
 RT randomly chosen clones from a marsupial mammary gland cDNA library.";
 RL Biochem. Genet. 32:181-190(1994).


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CC -1- FUNCTION: LACTOGLOBULIN IS THE PRIMARY COMPONENT OF WHEY, IT
CC BINDS RETINOL AND IS PROBABLY INVOLVED IN THE TRANSPORT OF
CC THAT MOLECULE.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY.
CC -----
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CC -----
DR EMBL: L14959; AAA31597.1; -.
DR EMBL: L14954; AAA31597.1; JOINED.
DR EMBL: L14955; AAA31597.1; JOINED.
DR EMBL: L14956; AAA31597.1; JOINED.
DR EMBL: L14957; AAA31597.1; JOINED.
DR EMBL: L14958; AAA31597.1; JOINED.
DR EMBL: X15212; CAA33282.1; -.
DR HSSP: P02734; 1BSY.
DR InterPro: IPR000566; Lipocalin_cytfabp.
DR Pfam: PF00061; Lipocalin; 1.
DR PROSITE: PS00213; LIPOCALIN; FALSE NEG.
KM Milk; Whey; Retinol-binding; Transport; Lipocalin; Signal.
FT SIGNAL 1 18 BY SIMILARITY.
FT CHAIN 1 174 BETA-LACTOGLOBULIN.
FT DISULFID 79 172 BY SIMILARITY.
FT DISULFID 122 134 BY SIMILARITY.
FT CONFLICT 76 76 A -> T (IN REF. 3).
SQ SEQUENCE 174 AA; 20219 MW; 6C5901051F99C991 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 RSKNDLG 44
Db 23 RSKNDLG 29

RESULT 5
TBA_PLAYO
ID TBA_PLAYO STANDARD; PRT; 197 AA.
AC P12343;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Tubulin alpha chain (Fragment).
OS Plasmodium berghei yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5862;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89014607; PubMed=2459618;
RA Akella R., Arasu P., Vaidya A.B.;
RT "Molecular clones of alpha-tubulin genes of Plasmodium yoelii reveal
RT an unusual feature of the carboxy terminus."
RL Mol. Biochem. Parasitol. 30:165-174(1988).
CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
CC BINDS TWO MOLES OF GTP. ONE AT AN EXCHANGEABLE SITE ON THE BETA
CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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CC -----
DR EMBL: M29816; AAA29779.1; -.
DR PIR: A54506; A54506.
DR InterPro: IPR000217; Tubulin.
DR InterPro: IPR003008; Tubulin_Fts2.
DR Pfam: PF00091; tubulin; 1.
DR PROSITE: PS00227; TUBULIN; PARTIAL.
KM Microtubules; GTP-binding.
FT NON_TER 1 1
SQ SEQUENCE 197 AA; 22111 MW; 4DAAE199CC6CD319 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 IKTKRSI 120
Db 82 IKTKRSI 88

RESULT 6
PRL_ICTPU
ID PRL_ICTPU STANDARD; PRT; 212 AA.
AC P51904; Q91819;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prolactin precursor (PRL).
GN PRL.
OS Itcalurus punctatus (channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RA Tang Y.;
RT "A study on the channel catfish (Ictalurus punctatus) growth hormone
RT gene family: structures of growth hormone and prolactin genes and
RT somatolactin cDNA, their evolutionary implications and expression in
RT the pituitary gland."
RL Thesis (1993), University of Maryland, U.S.A.
RN [2]
RP SEQUENCE OF 27-212 FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=93364578; PubMed=1308206;
RA Matsubae K., Igarashi A., Noso T., Chen T.T., Dunham R.A.,
RA Kawachi H.;
RT "Chemical identification of catfish growth hormone and prolactin."
RL Mol. Mar. Biol. Biotechnol. 1:239-249(1992).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PITUITARY GLANDS.
CC -1- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
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CC -----
DR EMBL: AF267990; AAF82287.1; -.
DR HSSP: Q28632; 1AN3.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF00103; hormone; 2.
DR PRINTS: PR00836; SOMATOTROPIN.
DR PROSITE: PS00266; SOMATOTROPIN_1; 1.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
KM Hormone; Pituitary; Signal.
FT SIGNAL 1 26
FT CHAIN 27 212 PROLACTIN.

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FT DISULFID 71 185 BY SIMILARITY.
FT DISULFID 202 212 BY SIMILARITY.
FT CONFLICT 91 91 G -> S (IN REF. 2).
FT CONFLICT 128 128 T -> S (IN REF. 2).
FT CONFLICT 203 203 D -> R (IN REF. 2).
SQ SEQUENCE 212 AA: 23365 MW: 073BF7B1DA573BE CRC64:

Query Match 1.6%; Score 7; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NDIGDN 47
Db 166 NDIGDN 172

RESULT 7
TBA_OCTVU
ID TBA_OCTVU STANDARD; PRT; 240 AA.
AC P24635;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tubulin alpha chain (Fragment).
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incurrata; Octopodidae; Octopus.
OX NCBI_TaxID=6645;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RA Zinov'Eva R.D., Alelnikova K.S., Tomarev S.I.;
RT "Isolation and structural characterization of cDNAs coding for alpha-
RT tubulin of the octopus eye lens."
RL Dokl. Akad. Nauk SSSR 302:462-467(1988).
CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
CC -----
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CC -----
DR EMBL; X15845; CAA33844.1; -
DR PIR; A61544; A61544.
DR InterPro; IPR000217; Tubulin.
DR InterPro; IPR003008; Tubulin_Ftsz.
DR Pfam; PF00091; tubulin.1.
DR PROSITE; PS00227; TUBULIN; PARTIAL.
KW Microtubules; GTP-binding.
FT NON_TER 1
FT SITE 240 GN 240 INVOLVED IN POLYMERIZATION.
SQ SEQUENCE 240 AA: 26961 MW: 13BB3A1F740F2416 CRC64:

Query Match 1.6%; Score 7; DB 1; Length 240;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 IKTKRSI 120
Db 124 IKTKRSI 130

RESULT 8
Y04_MYCPN
ID Y04_MYCPN STANDARD; PRT; 270 AA.
AC P73355;

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DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical ABC transporter ATP-binding protein MG304 homolog
DE (A05_orf270L).
GN MPN433 OR MP408.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129.
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelfeich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae."
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
CC -----
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CC -----
DR EMBL; AE000040; AAB96056.1; -
DR InterPro; IPR003593; AAA_Arpase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran.1.
DR Prodom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA.1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW Hypothetical protein; ATP-binding; Transport; Complete proteome.
FT NP_BIND 36 43 ATP (POTENTIAL).
SQ SEQUENCE 270 AA: 30770 MW: 6512640E4BC051B4 CRC64:

Query Match 1.6%; Score 7; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 KQFTPLS 174
Db 125 KQFTPLS 131

RESULT 9
ILVE_THEMEA
ID ILVE_THEMEA STANDARD; PRT; 273 AA.
AC P74921;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable branched-chain amino acid aminotransferase (EC 2.6.1.42)
DE (BCAT).
DE ILVE OR TM0831.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
OC Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.W.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from

```

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RT genome sequence of Thermotoga maritima."
RL Nature 399:323-329(1999).
RN [2]
RP SEQUENCE OF 68-273 FROM N.A.
RC STRAIN-MSB / DSM 3109;
RX MEDLINE-97017137; PubMed-8863738;
RA Guipaud O., Labedan B., Forterre P.;
RT "A gyrB-like gene from the hyperthermophilic bacterium Thermotoga
maritima."
RL Gene 174:121-128(1996).
CC -1- FUNCTION: Acts on leucine, isoleucine and valine (by similarity).
CC -1- CATALYTIC ACTIVITY: L-leucine + 2-oxoglutarate -> 4-methyl-2-
CC oxopentanoate + L-glutamate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: Valine and isoleucine biosynthesis.
CC -1- SIMILARITY: BELONGS TO CLASS-IV OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
-----
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-----
DR EMBL: AE001750; AAD35913.1; -.
DR EMBL: U49692; AAC44497.1; -.
DR HSSP: P00510; 1A3G.
DR TIGR: TM0831; -.
DR InterPro: IPR001544; AminoTran_4.
DR Pfam: PF01063; aminotran_4; 1.
DR ProDom: PD001961; AminoTran_4; 1.
DR PROSITE: PS00770; AA_TRANSF_1; 1.
DR TRANSFAR: AminoTran; Branched-chain amino acid biosynthesis;
DR Pyridoxal phosphate; Complete proteome.
FT CONFLICT 77 A -> R (IN REF. 2).
FT SEQUENCE 273 AA; 31158 MW; 2162B705612E90B3 CRC64;
SQ
Query Match 1.6%; Score 7; DB 1; Length 273;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 PLSLSPD 178
Db 61 PLSLSFD 67
-----
RESULT 10
MIAA_PSEPU STANDARD; PRT; 322 AA.
AC 030762;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (IP
DE transferase) (isopentenyl-diphosphate:tRNA isopentenyltransferase)
DE (IPTrase) (IPTr).
DE MIAA.
GN Pseudomonas putida.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN-M.
RA Olekhnovich I.N., Gusein G.N.;
RT "Attenuation of the Pseudomonas putida trpE and trpDC genes."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE FIRST STEP IN THE BIOSYNTHESIS OF
CC 2-METHYLTIO-56-(DELTA(2)-ISOPENTENYL)-ADENOSINE (MS121I[6(A)])
CC ADJACENT TO THE ANTICODON OF SEVERAL tRNA SPECIES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: isopentenyl diphosphate + tRNA -> diphosphate +

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CC tRNA containing 6-isopentenyladenosine.
CC -1- SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
-----
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-----
DR EMBL: AF016312; AAB69443.1; -.
DR InterPro: IPR002627; IPPT.
DR Pfam: PF01715; IPPT; 1.
DR ProDom: PD004674; IPPT; 1.
DR TIGRPFAM: TIGR00174; mlaa; 1.
DR TRANSFAR: Nucleotidyltransferase; tRNA processing; ATP-binding.
FT NF_BIND 12 19 ATP (POTENTIAL).
FT SEQUENCE 322 AA; 35488 MW; D1AA81A2D7B32F6A CRC64;
SQ
Query Match 1.6%; Score 7; DB 1; Length 322;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 FVDEVRS 39
Db 231 FVDEVRS 237
-----
RESULT 11
SPL_BACBR STANDARD; PRT; 326 AA.
AC P43131;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Protease inhibitor precursor (BBRP1).
DE Bacillus brevis.
OS Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
OX NCBI_TaxID=1393;
OX [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-32; 104-112 AND 122-136.
RC STRAIN=HPD31;
RX MEDLINE-92304060; PubMed-1610177;
RA Shiga Y., Hasegawa K., Tsuboi A., Yamagata H., Ueda S.;
RT "Characterization of an extracellular protease inhibitor of Bacillus
RT brevis HPD31 and nucleotide sequence of the corresponding gene."
RL Appl. Environ. Microbiol. 58:525-531(1992).
CC -1- FUNCTION: SHOWS INHIBITORY ACTIVITY TOWARDS SERINE PROTEASES, SUCH
CC AS TRYPSIN, CHYMOTRYPSIN, AND SUBTILISIN. MAY FORM A TRYPSIN-
CC INHIBITOR COMPLEX IN A MOLAR RATIO OF 1:1. IT IS HEAT RESISTANT AT
CC NEUTRAL AND ACIDIC pHs.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: MAY UNDERGO ACTIVATION AFTER SECRETION. IT IS PRODUCED
CC EXTRACELLULARLY IN MULTIPLE FORMS HAVING AT LEAST THREE DIFFERENT
CC MOLECULAR WEIGHTS (BBRP1-A, -B, AND -C).
-----
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-----
DR EMBL: D10696; BAA01538.1; -.
KM Serine protease inhibitor; Protease inhibitor; Signal; Repeat.
FT STGNAL 1 24
FT CHAIN 25 326 SERINE PROTEASE INHIBITOR.
FT CHAIN 104 326 SERINE PROTEASE INHIBITOR-C.
FT CHAIN 104 7 SERINE PROTEASE INHIBITOR-B (POTENTIAL).
FT CHAIN 122 326 SERINE PROTEASE INHIBITOR-A.
FT DOMAIN 177 304 CONTAINS TWO APPROXIMATE REPEATS.

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ET REPEAT 177 208 1.
FT REPEAT 272 304 2.
SQ SEQUENCE 326 AA; 35100 MW; 1C0456BAFA912F77 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 326;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 30 PVAFVDE 36
    |||||
DB 119 PVAFVDE 125

RESULT 12
FLAD_METUA STANDARD; PRT; 342 AA.
AC 058305;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative flagella-related protein D.
GN FLAD OR Mj0895.
OS Methanococcus jannaschlii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Ullrich T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschlii.
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: STRONG, TO M.VOLTAE FLAD, ALSO TO FLAE.
CC -----
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CC -----
CC
CC EMBL; U67533; AAB98748.1; -.
DR TIGR; Mj0895; -.
KW Flagella; Complete proteome.
SQ SEQUENCE 342 AA; 39950 MW; B384DDE1775566C CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 342;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PDILDYX 362
    |||||
DB 255 PDILDYX 261

RESULT 13
Y755_METUA STANDARD; PRT; 342 AA.
AC 058163;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein Mj0755 precursor.

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GN Mj0755.
OS Methanococcus jannaschlii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Ullrich T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschlii.
RL Science 273:1058-1073(1996).
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CC -----
CC
CC EMBL; U67521; AAB98748.1; -.
DR TIGR; Mj0755; -.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 18
FT CHAIN 19 342
FT STRAIN JAL-1 / DSM 2661 / ATCC 43067;
SQ SEQUENCE 342 AA; 38778 MW; BD25220A7EBAD85C CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 342;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 YTTALEN 82
    |||||
DB 90 YTTALEN 96

RESULT 14
AMT_AOUAE STANDARD; PRT; 423 AA.
AC 066515;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable ammonium transporter.
GN AMT OR AMTB OR AO_112.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus".
RL Nature 392:353-358(1998).
CC -1- FUNCTION: INVOLVED IN THE UPTAKE OF AMMONIA (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- SIMILARITY: BELONGS TO THE AMT1/MEP/NRGA FAMILY OF AMMONIUM
CC TRANSPORTERS (TC 2.49).

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CC -----
 DR EMBL; AE000674; AAC06478.1; -
 DR InterPro: IPR001905; Ammonium_transp.
 DR Pfam; PF00909; Ammonium_transp; 1.
 DR TIGRFAMs; TIGR00836; ant; 1.
 DR PROSITE; PS01219; AMMONIUM_TRANSP; 1.
 KW Transport; Transmembrane; Complete proteome.
 FT TRANSMEM 3 23 POTENTIAL.
 FT TRANSMEM 31 51 POTENTIAL.
 FT TRANSMEM 64 84 POTENTIAL.
 FT TRANSMEM 123 143 POTENTIAL.
 FT TRANSMEM 150 170 POTENTIAL.
 FT TRANSMEM 183 203 POTENTIAL.
 FT TRANSMEM 217 237 POTENTIAL.
 FT TRANSMEM 246 266 POTENTIAL.
 FT TRANSMEM 278 298 POTENTIAL.
 FT TRANSMEM 301 321 POTENTIAL.
 FT TRANSMEM 331 351 POTENTIAL.
 FT TRANSMEM 374 394 POTENTIAL.
 SQ SEQUENCE 423 AA; 44322 MW; 166203BBB2A8A15B CRC64;

Query Match 1.6%; Score 7; DB 1; Length 423;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 402 LGKISG 408
 |||||
 Db 104 LGKISG 110

RESULT 15
 TBA_ONCKE STANDARD; PRT; 444 AA.
 AC P30436;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Tubulin alpha chain.
 OS Oncorhynchus keta (Chum salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8018;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93208376; PubMed=1296820;
 RA Coe I.R., Munro R., Sherwood N.M.;
 RT "Isolation of different brain-specific isoforms of alpha-tubulins
 RL from chum salmon (Oncorhynchus keta).";
 RL DNA Seq. 3:257-262(1992).
 CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
 CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
 CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
 CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
 CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
 CC -----
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CC -----
 DR EMBL; X66973; CAA47384.1; -

DR PIR; S25004; S25004.
 DR InterPro: IPR000217; Tubulin.
 DR InterPro: IPR003008; Tubulin_Fts2.
 DR Pfam; PF00091; tubulin; 1.
 DR PRINTS; PR01161; TUBULIN.
 DR PROSITE; PS00227; TUBULIN; 1.
 KW Microtubules; GTP-binding; Multigene family.
 FT NP_BIND 136 142 GTP (POTENTIAL).
 FT SITE 444 444 INVOLVED IN POLYMERIZATION.
 SQ SEQUENCE 444 AA; 49314 MW; C2CD75432DD6BAF CRC64;

Query Match 1.6%; Score 7; DB 1; Length 444;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 IKTKRSI 120
 |||||
 Db 329 IKTKRSI 335

Search completed: November 12, 2002, 11:45:28
 Job time : 9.5 secs

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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:46 ; Search time 26.25 Seconds
(without alignments)
3469,441 Million cell updates/sec

Title: US-09-787-083-4

Perfect score: 442

Sequence: 1 MKVSLSTLTSLPCFALIA.....YNHATSFVGLMLNDMGL 442

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_todent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	2.0	382	09K0U7	09K0U7 neisseria m
2	9	2.0	409	09J721	09J721 neisseria m
3	9	2.0	862	09C162	09C162 pasteurella
4	9	2.0	1432	09AX85	09AX85 oryza sativ
5	8	1.8	227	08TUS3	08TUS3 methanopyru
6	8	1.8	299	09M268	09M268 arabidopsis
7	8	1.8	306	09C122	09C122 pasteurella
8	8	1.8	415	0942C0	0942C0 isoeetes dur
9	8	1.6	55	067608	067608 tomato gold
10	7	1.6	68	092FV7	092FV7 rickettsia
11	7	1.6	72	091ZS4	091ZS4 potato viru
12	7	1.6	72	091ZS5	091ZS5 potato viru
13	7	1.6	95	091ZS3	091ZS3 potato viru
14	7	1.6	96	091ZS8	091ZS8 potato viru
15	7	1.6	101	091ZS6	091ZS6 potato viru
16	7	1.6	112	092HS2	092HS2 rickettsia

17	7	1.6	122	09RU16	09RU16 deinococcus
18	7	1.6	124	091ZS7	091ZS7 potato viru
19	7	1.6	131	09GMD4	09GMD4 macaca fusc
20	7	1.6	138	091ZQ7	091ZQ7 potato viru
21	7	1.6	147	036035	036035 hexamita in
22	7	1.6	158	0929C1	0929C1 chlamydia p
23	7	1.6	164	097JH4	097JH4 clostridium
24	7	1.6	169	09L2A7	09L2A7 streptomyc
25	7	1.6	186	09LXR9	09LXR9 arabidopsis
26	7	1.6	189	09DF12	09DF12 notothenia
27	7	1.6	194	0920K4	0920K4 rhizobium m
28	7	1.6	198	09BUX9	09BUX9 homo sapien
29	7	1.6	200	08R2L3	08R2L3 dictyostel
30	7	1.6	212	0930ZNS	0930ZNS heteropneus
31	7	1.6	216	09X6H6	09X6H6 streptococ
32	7	1.6	218	09RF14	09RF14 streptococ
33	7	1.6	219	017594	017594 caenorhabdi
34	7	1.6	220	09XCK1	09XCK1 streptococ
35	7	1.6	220	036036	036036 spiroplasma
36	7	1.6	221	065002	065002 alfalfa mos
37	7	1.6	227	09BWF4	09BWF4 glossina mo
38	7	1.6	233	09M2B0	09M2B0 ovis aries
39	7	1.6	233	08YH08	08YH08 bruceella me
40	7	1.6	236	09DFE8	09DFE8 notothenia
41	7	1.6	264	085260	085260 potato viru
42	7	1.6	265	038155	038155 bacterioph
43	7	1.6	267	091N40	091N40 potato viru
44	7	1.6	267	099363	099363 bacterioph
45	7	1.6	267	086842	086842 potato viru

ALIGNMENTS

RESULT 1
ID 09K0U7 PRELIMINARY: PRT: 382 AA.
AC 09K0U7: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Phospholipase A1, putative.
GN MMB0464.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettein H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Clifton H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scariato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
RL Science 287:1809-1815(2000).
DR EMBL: AE002403; AAF40901.1; -.
DR HSSP: P00631; IQD5.
DR TIGR: NMB0464; -.
DR InterPro: IPR003187; PLA1.
DR Pfam: PF02253; PLA1; 1.
SO Complete proteome.
SQ SEQUENCE 382 AA; 42714 MW; B468A802F062E836 CRC64;
Query Match 2.0%; Score 9; DB 16; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 279 PEIFLTPV 287
 |||||||
 Db 221 PEIFLTPV 229

RESULT 2

O9JUT21 PRELIMINARY; PRT; 409 AA.
 ID O9JUT21
 AC O9JUT21
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative phospholipase.
 GN NMA2021.
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
 RX MEDLINE=2022556; PubMed=10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagers K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrall B.G.;
 RA "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491";
 RT Nature 404:502-506(2000).
 RL EMBL; AL162757; CAB85240.1; -.
 DR HSSP; P00631; 10D5.
 DR InterPro; IPR003187; PLA1.
 DR Pfam; PF02253; PLA1; 1.
 KW Complete proteome.
 SQ SEQUENCE 409 AA; 45862 MW; CD6585B064D01A41 CRC64;

Query Match 2.0%; Score 9; DB 16; Length 409;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 279 PEIFLTPV 287
 |||||||
 Db 248 PEIFLTPV 256

RESULT 3

O9CL62 PRELIMINARY; PRT; 862 AA.
 ID O9CL62
 AC O9CL62
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE CvgSY.
 GN CvgSY OR PM1380.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitam T.S., Kapur V.;
 RT "Complete sequence of Pasteurella multocida pm70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 CC -1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULATORY COMPONENTS OF SENSOR TRANSDUCTION SYSTEMS.
 CC -1- SIMILARITY: AA03464.1; -.
 DR EMBL; AE006176; AA03464.1; -.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR004358; Bact_sens_pt_C.
 DR InterPro; IPR003660; HAMF.

DR InterPro; IPR003661; His_kinA.
 DR InterPro; IPR004359; His_kin_sig.
 DR InterPro; IPR001789; Response_reg.
 DR Pfam; PF00672; HAMF; 1.
 DR Pfam; PF02518; HATPase_C; 1.
 DR Pfam; PF00072; response_reg; 1.
 DR Pfam; PF00512; signal; 1.
 DR PRINTS; PR00344; BCTRLSENSOR.
 DR ProDom; PD000039; Response_reg; 1.
 DR SMART; SM00304; HAMF; 1.
 DR SMART; SM00387; HATPase_C; 1.
 DR SMART; SM00388; HisKA; 1.
 DR SMART; SM00446; REC; 1.
 KW Kinase; Phosphorylation; Sensory transduction; Transferase;
 KW Complete proteome.
 SQ SEQUENCE 862 AA; 97846 MW; AB681A3B63626C0 CRC64;

Query Match 2.0%; Score 9; DB 16; Length 862;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LSTLTLSTL 13
 |||||||
 Db 293 LSTLTLSTL 301

RESULT 4

O9AX85 PRELIMINARY; PRT; 1432 AA.
 ID O9AX85
 AC O9AX85
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative ABC transporter protein.
 GN P0410E03.7.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone: P0410E03.";
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AP002844; BAB21276.1; -.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transportr.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD00006; ABC_transportr; 1.
 DR SMART; SM00382; AAA; 2.
 KW ATP-binding.
 SQ SEQUENCE 1432 AA; 160234 MW; 04B8CF2CAA08D993 CRC64;

Query Match 2.0%; Score 9; DB 10; Length 1432;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 170 FTPLSLSPD 178
 |||||||
 Db 830 FTPLSLSPD 838

RESULT 5

O8TUS3 PRELIMINARY; PRT; 227 AA.
 ID O8TUS3
 AC O8TUS3
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Predicted phosphatase of the PHP family.

GN MK1681.
 OS Methanopyrus kandleri.
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
 OC Methanopyrus.
 OX NCBI_TaxID=2320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AV19 / DSM 6324 / JCM 9639;
 RX MEDLINE=21927647; PubMed=11930014;
 RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
 RA Shcherbina O.V., Shakhova V.V., Belova G.I., Aravind L.,
 RA Nale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
 RA Malykh A.G., Koonin E.V., Kozhavkin S.A.;
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
 and monophyly of archaeal methanogens.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
 DR EMBL; AE010457; AA02894.1; -;
 KW Complete proteome.
 SQ SEQUENCE 227 AA; 24975 MW; B80099EBE2BA8912 CRC64;

Query Match 1.8%; Score 8; DB 17; Length 227;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 LVHGETPA 112
 |||||
 DB 106 LVHGETPA 113

RESULT 6
 O9M268 PRELIMINARY; PRT; 299 AA.

AC O9M268;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE RAV-like protein.
 GN F21F14.140.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Choinsne N., Robert C., Brottier P., Wincker P., Cactolico L.,
 RA Attiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X., Queller F., Salanoubat M.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA ED Arabidopsis sequencing project;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL138642; CAB71904.1; -;
 DR InterPro: IPR003340; TF_B3.
 DR Pfam: PF02362; B3; 1
 SQ SEQUENCE 299 AA; 34270 MW; 2AB841F179DD174B CRC64;

Query Match 1.8%; Score 8; DB 10; Length 299;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 174 SLSPDLDR 181
 |||||
 DB 292 SLSPDLDR 299

RESULT 7
 O9CL22 PRELIMINARY; PRT; 306 AA.
 AC O9CL22;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical protein PM1426.
 GN PM1426.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida Pm70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL; AE006179; AK03510.1; -;
 DR HSSP; P00631; 10D6.
 DR InterPro: IPR003187; PLA1.
 DR Pfam: PF02253; PLA1; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 306 AA; 35580 MW; EAF3DE8C1C2B26E CRC64;

Query Match 1.8%; Score 8; DB 16; Length 306;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 314 KLSRSMNR 321
 |||||
 DB 184 KLSRSMNR 191

RESULT 8

O94ZC0 PRELIMINARY; PRT; 415 AA.

AC O94ZC0;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE NADH dehydrogenase subunit 2 (Fragment).
 GN NAD2.
 OS Isoetes duriei.
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Lycopodiophyta; Isoetopsida; Isoetales; Isoetaceae; Isoetes.
 OX NCBI_TaxID=56743;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Knopf V.;
 RT "An extended molecular land plant phylogeny.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CAPALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 DR EMBL; AJ409119; CAC50076.1; -;
 DR InterPro: IPR001750; Oxidored_g1.
 DR InterPro: IPR003880; Pantine_attach.
 DR Pfam: PF00361; Oxidored_g1; 1.
 DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
 KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 415 AA; 45082 MW; E0D3AC7820F6309 CRC64;

Query Match 1.8%; Score 8; DB 8; Length 415;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LSTLTSLI 12
 |||||
 DB 341 LSTLTSLI 348

RESULT 9
 O67608 PRELIMINARY; PRT; 55 AA.
 ID O67608
 AC O67608;

DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last annotation update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Tomato golden mosaic virus subgenomic DNA derived from DNA B cccds -
 DE covalently closed circular double-stranded molecule.
 OS Tomato golden mosaic virus (TMGV).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=10831;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87040767; PubMed=3022243;
 RA MacDowell S.W., Coutts R.H.A., Buck K.W.;
 RT "Molecular characterization of subgenomic single-stranded and double-
 RT stranded DNA forms isolated from plants infected with tomato golden
 RT mosaic virus."
 RL Nucleic Acids Res. 14:7967-7984(1986).
 DR EMBL: X04485; CA28171.1; -;
 DR InterPro: IPR000211; Gemin1.BL.
 DR Pfam: PF00845; Gemin1.BL; 1.
 SQ SEQUENCE 55 AA; 6281 MW; 41963570D739EC96.CRC64;

Query Match 1.6%; Score 7; DB 12; Length 55;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 312 SAKISRS 318
 Db 43 SAKISRS 49

RESULT 10
 O92PV7 PRELIMINARY; PRT; 68 AA.
 AC O92PV7;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Hypothetical protein RC1370.
 GN RC1370.
 OS Rickettsia conorii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OC NCBI_TaxID=781;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MALISH 7;
 RX MEDLINE=21442074; PubMed=11557893;
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-F., Barde V.,
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
 RA Reault D.;
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."
 RL Science 293:2093-2098(2001).
 DR EMBL: AE008682; AAL03908.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 68 AA; 7373 MW; 9BF44F56AE48E66.CRC64;

Query Match 1.6%; Score 7; DB 16; Length 68;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 TALENKT 84
 Db 45 TALENKT 51

RESULT 11
 O91ZS4 PRELIMINARY; PRT; 72 AA.
 AC O91ZS4;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Coat protein (Fragment).

GN CP.
 OS Potato virus Y strain NTN (PVY(NTN)).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OC NCBI_TaxID=122280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUBER NECROSING;
 RA Cerovska N., Filigayova M., Moravec T., Petrzik K.;
 RT "Differences in nucleotide and amino acid sequences of N-terminal
 RT parts of coat proteins among isolates of potato virus Y-NTN strain."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF228634; AAF67875.1; -;
 DR InterPro: IPR001592; Poly-coat.
 DR Pfam: PF00767; Poly-coat; 1.
 FT NON_TER 1 72
 FT NON_TER 1 72
 SQ SEQUENCE 72 AA; 7692 MW; 4F129B870523B482.CRC64;

Query Match 1.6%; Score 7; DB 12; Length 72;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 156 TKDKAQ 162
 Db 11 TKDKAQ 17

RESULT 12
 O91ZS5 PRELIMINARY; PRT; 72 AA.
 AC O91ZS5;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Coat protein (Fragment).
 GN CP.
 OS Potato virus Y strain NTN (PVY(NTN)).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OC NCBI_TaxID=122280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUBER NECROSING;
 RA Cerovska N., Filigayova M., Moravec T., Petrzik K.;
 RT "Differences in nucleotide and amino acid sequences of N-terminal
 RT parts of coat proteins among isolates of potato virus Y-NTN strain."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF228633; AAF67874.1; -;
 DR InterPro: IPR001592; Poly-coat.
 DR Pfam: PF00767; Poly-coat; 1.
 FT NON_TER 1 72
 FT NON_TER 1 72
 SQ SEQUENCE 72 AA; 7721 MW; 2C5287E15624C8D.CRC64;

Query Match 1.6%; Score 7; DB 12; Length 72;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 156 TKDKAQ 162
 Db 11 TKDKAQ 17

RESULT 13
 O91ZS3 PRELIMINARY; PRT; 95 AA.
 AC O91ZS3;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Coat protein (Fragment).
 GN CP.

```

OS   Potato virus Y strain NTN (PVY(MTN)).
OC   Viruses: ssRNA positive-strand viruses, no DNA stage: Potyviridae;
OC   Potyvirus.
OX   NCBI_TaxID=122280;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TUBER NECROSING;
RA   Cerovska N., Filigayova M., Moravec T., Petrzik K.;
RT   "Differences in nucleotide and amino acid sequences of N-terminal
RT   parts of coat proteins among isolates of potato virus Y-NTN strain.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR   EMBL: AF228635; AAF67876.1; -.
DR   InterPro: IPR001592; Poty_coat.
DR   Pfam: PF00767; Poty_coat; 1.
FT   NON_TER 1 95
FT   NON_TER 95 95
SQ   SEQUENCE 95 AA; 10446 MW; 28C0689177C9928 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   156 TKKDAKQ 162
      |||||
Db    11 TKKDAKQ 17

RESULT 14
Q91ZS8 PRELIMINARY; PRT; 96 AA;
AC   Q91ZS8;
DT   01-OCT-2000 (TREMBlrel. 15, Created)
DT   01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT   01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE   Coat protein (Fragment).
GN   CP.
OS   Potato virus Y (strain N) (PVY).
OC   Viruses: ssRNA positive-strand viruses, no DNA stage: Potyviridae;
OC   Potyvirus.
OX   NCBI_TaxID=12219;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NECROSING;
RA   Cerovska N., Filigayova M., Moravec T., Petrzik K.;
RT   "Differences in nucleotide and amino acid sequences of N-terminal
RT   parts of coat proteins among isolates of potato virus Y-NTN strain.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR   EMBL: AF228630; AAF67871.1; -.
DR   InterPro: IPR001592; Poty_coat.
DR   Pfam: PF00767; Poty_coat; 1.
FT   NON_TER 1 96
FT   NON_TER 96 96
SQ   SEQUENCE 96 AA; 10559 MW; 89C3A5675B9784CA CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   156 TKKDAKQ 162
      |||||
Db    11 TKKDAKQ 17

RESULT 15
Q91ZS6 PRELIMINARY; PRT; 101 AA.
AC   Q91ZS6;
DT   01-OCT-2000 (TREMBlrel. 15, Created)
DT   01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT   01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE   Coat protein (Fragment).
GN   CP.
OS   Potato virus Y strain NTN (PVY(MTN)).

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OC   Viruses: ssRNA positive-strand viruses, no DNA stage: Potyviridae;
OC   Potyvirus.
OX   NCBI_TaxID=122280;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TUBER NECROSING;
RA   Cerovska N., Filigayova M., Moravec T., Petrzik K.;
RT   "Differences in nucleotide and amino acid sequences of N-terminal
RT   parts of coat proteins among isolates of potato virus Y-NTN strain.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR   EMBL: AF228632; AAF67873.1; -.
DR   InterPro: IPR001592; Poty_coat.
DR   Pfam: PF00767; Poty_coat; 1.
FT   NON_TER 1 101
FT   NON_TER 101 101
SQ   SEQUENCE 101 AA; 11112 MW; B55BF51C3D5FE9BD CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 101;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   156 TKKDAKQ 162
      |||||
Db    11 TKKDAKQ 17

```

Search completed: November 12, 2002, 11:48:23
 Job time : 28.25 secs

1
-
6

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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:40 ; Search time 30 Seconds
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Title: US-09-787-083-6

Perfect score: 442
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Scoring table: OLIGO

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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9	/SID2/gcgdata/genseq/genseqp-emb1/AA1988.DAT *
10	/SID2/gcgdata/genseq/genseqp-emb1/AA1989.DAT *
11	/SID2/gcgdata/genseq/genseqp-emb1/AA1990.DAT *
12	/SID2/gcgdata/genseq/genseqp-emb1/AA1991.DAT *
13	/SID2/gcgdata/genseq/genseqp-emb1/AA1992.DAT *
14	/SID2/gcgdata/genseq/genseqp-emb1/AA1993.DAT *
15	/SID2/gcgdata/genseq/genseqp-emb1/AA1994.DAT *
16	/SID2/gcgdata/genseq/genseqp-emb1/AA1995.DAT *
17	/SID2/gcgdata/genseq/genseqp-emb1/AA1996.DAT *
18	/SID2/gcgdata/genseq/genseqp-emb1/AA1997.DAT *
19	/SID2/gcgdata/genseq/genseqp-emb1/AA1998.DAT *
20	/SID2/gcgdata/genseq/genseqp-emb1/AA1999.DAT *
21	/SID2/gcgdata/genseq/genseqp-emb1/AA2000.DAT *
22	/SID2/gcgdata/genseq/genseqp-emb1/AA2001.DAT *
23	/SID2/gcgdata/genseq/genseqp-emb1/AA2002.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	442	100.0	442	21	AAV852270	BASB034 amino acid
2	390	88.2	442	21	AAV85269	BASB034 amino acid
3	316	71.5	442	21	AAV85271	BASB034 amino acid
4	224	50.7	289	23	AAO17569	M catarrhalis MCAH
5	224	50.7	289	23	AAV85268	BASB034 amino acid
6	9	2.0	255	22	ABG18034	Novel human diagen
7	9	2.0	370	21	AAV75156	Neisseria gonorrhoe
8	9	2.0	370	21	AAV75157	Neisseria meningit
9	9	2.0	370	21	AAV75158	Neisseria meningit
10	9	2.0	374	21	AAV70629	Neisseria meningit

11	9	2	0	375	21	AAV70628	Neisseria meningitidis
12	8	1	8	278	21	AAG11137	Arabisopsis thaliana
13	8	1	8	283	21	AAG11136	Arabisopsis thaliana
14	8	1	8	289	21	AAG11135	Arabisopsis thaliana
15	7	1	6	16	15	AAK52127	Mouse light chain
16	7	1	6	33	22	AAK75069	Human colon cancer
17	7	1	6	50	21	AAV79483	Rat alpha tubulin
18	7	1	6	64	21	AAK06322	Arabisopsis thaliana
19	7	1	6	75	22	AAU22329	Human cardiovascular
20	7	1	6	82	21	AAK01488	Human secreted protein
21	7	1	6	88	22	AAK03041	Human polypeptide
22	7	1	6	108	21	AAK37811	Arabisopsis thaliana
23	7	1	6	110	22	AAK03010	Human polypeptide
24	7	1	6	114	22	AAK55952	Protonobacterium
25	7	1	6	114	22	AAK02870	Human polypeptide
26	7	1	6	116	21	AAK87313	Human signal peptidase
27	7	1	6	116	23	AAK65204	Human albumin fushi
28	7	1	6	116	23	AAK65205	Human albumin fushi
29	7	1	6	116	23	AAK65206	Human albumin fushi
30	7	1	6	116	23	AAU91093	Human secreted protein
31	7	1	6	116	23	AAU91120	Human secreted protein
32	7	1	6	116	23	AAU91121	Human secreted protein
33	7	1	6	116	23	AAK53721	Lactococcus lactis
34	7	1	6	136	21	AAK37810	Arabisopsis thaliana
35	7	1	6	157	21	AAK29867	Arabisopsis thaliana
36	7	1	6	162	23	AAK42371	Human ovarian anti
37	7	1	6	169	20	AAV34661	Chlamydia pneumoniae
38	7	1	6	181	21	AAK37809	Arabisopsis thaliana
39	7	1	6	181	23	AAK42926	Human ovarian anti
40	7	1	6	214	22	AAK65814	Drosophila melanogaster
41	7	1	6	221	23	AAK68403	Alfalfa mosaic virus
42	7	1	6	256	22	AAK25462	Human mdm2 protein
43	7	1	6	268	13	AAK21542	Envelope protein of
44	7	1	6	302	13	AAK4254	Protease inhibitor
45	7	1	6	316	21	AAK39500	Arabisopsis thaliana

ALIGNMENTS

```

RESULT 1
AAy85270
ID      AAY85270 standard; Protein; 442 AA.
XX
XX      AAY85270;
AC
XX
XX      29-JUN-2000 (first entry)
DT
XX
XX      BASB034 amino acid sequence #3.
DE
XX
XX      Moraxella catarrhalis infection; BASB034; diagnosis; staging;
XX      vaccine; bacteriostatic; treatment; prevention; otitis media;
XX      sinusitis; nosocomial infection; invasive disease; chronic otitis
XX      hearing loss; antibacterial drug.
XX
XX      Moraxella catarrhalis.
OS
XX
XX      WO200015802-A1.
XX
XX      23-MAR-2000.
PD
XX
XX      14-SEP-1999; 99WO-EP06781.
PF
XX
XX      14-SEP-1998; 98GB-0020002.
PR
XX
XX      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX
XX      Ruelle J;
PI
XX
XX      WPI: 2000-271440/23.
DR
XX      N-PSDB: AAA10702.
XX
XX      Novel BASB034 polynucleotides and polypeptides from Moraxella
PT

```

PT catarrhalis used to prepare vaccines against bacterial infections -
XX
PS Claim 3; Page 68; 106pp; English.
XX
CC This sequence represents a Moraxella catarrhalis BASB034 polypeptide from
CC strain Mc2913. The invention relates to BASB034 polypeptides from
CC M. catarrhalis strains Mc2931, Mc2908, Mc2913 and Mc2969. The BASB034
CC polynucleotides and polypeptides may be employed as research reagents and
CC material for the discovery of treatments and diagnostics for diseases,
CC particularly human diseases. They are particularly used to diagnose and
CC treat M. catarrhalis infections. They can be used for diagnosis of
CC disease, staging of disease, or determining response of an infectious
CC organism to drugs. The polynucleotides may be used as a source for
CC hybridization probes, and for screening of genetic mutations, serotype,
CC organism or strain identification, identification of mutations in BASB034
CC sequences, and as components of arrays which are useful for diagnostic
CC and prognostic purposes. The polypeptides can be used to produce
CC antibodies. The polypeptides can also be used in vaccine formulations,
CC and to identify agonists and antagonists. The polypeptides, antibodies,
CC agonists and antagonists (which are bacteriostatic) are used for the
CC treatment and prevention of diseases such as otitis media in infants and
CC children, pneumonia in elderlies, sinusitis, nosocomial infections and
CC invasive diseases, and chronic otitis media with hearing loss. The
CC polypeptides, agonists and antagonists are also used for screening of
CC antibacterial drugs. The BASB034 products of the invention can be used
CC screen for new antibacterial compounds that may target resistant
CC bacteria.
XX
SQ Sequence 442 AA;
XX
Query Match 100.0%; Score 442; DB 21; Length 442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKVSLSTLTSTLSCFPLATQAKAVNPVAFYDEVSENDLQDNELPIDVQSATQSA 60
DB 1 MKVSLSTLTSTLSCFPLATQAKAVNPVAFYDEVSENDLQDNELPIDVQSATQSA 60
QY 61 STDYANPLDEHEPELYTALLENKTMILNCSALNODIMRLACYDTLVHGETPAVITKRSI 120
DB 61 STDYANPLDEHEPELYTALLENKTMILNCSALNODIMRLACYDTLVHGETPAVITKRSI 120
QY 121 RLDETTIMQTIKGRQVYVYQETTDPIFLMGNEKGMILTKKDAKOLEYAAKQFTPLSFDLD 180
DB 121 RLDETTIMQTIKGRQVYVYQETTDPIFLMGNEKGMILTKKDAKOLEYAAKQFTPLSFDLD 180
QY 181 RNNTPPLMSSRPNNPMYVLPITFMHGKPNRSPPTPSHEARQFTPNRPAPELKFQVSVKYKA 240
DB 181 RNNTPPLMSSRPNNPMYVLPITFMHGKPNRSPPTPSHEARQFTPNRPAPELKFQVSVKYKA 240
QY 241 AEDLMGTDSDLMFGYTOQSHMOIFNGKNSRPFYVHDYQPEFLTPQPVYSDLPMDGKYVMI 300
DB 241 AEDLMGTDSDLMFGYTOQSHMOIFNGKNSRPFYVHDYQPEFLTPQPVYSDLPMDGKYVMI 300
QY 301 GMGAVHNSNGESAKLSNSMNRAYLMAEMENKLTVMPIRIGRIKESGSGQDDNPDLILD 360
DB 301 GMGAVHNSNGESAKLSNSMNRAYLMAEMENKLTVMPIRIGRIKESGSGQDDNPDLILD 360
QY 361 YYGVDVRFYLOLENKNSISTVYRNPSSGALQLODVYVPLGIGISYFPIPGYQGS 420
DB 361 YYGVDVRFYLOLENKNSISTVYRNPSSGALQLODVYVPLGIGISYFPIPGYQGS 420
QY 421 IDYNHEATSPFGVGLMDNMGL 442
DB 421 IDYNHEATSPFGVGLMDNMGL 442

DT 29-JUN-2000 (first entry)
XX
DE BASB034 amino acid sequence #2.
XX
KW Moraxella catarrhalis infection; BASB034; diagnosis; staging;
KW vaccine; bacteriostatic; treatment; prevention; otitis media; pneumonia;
KW sinusitis; nosocomial infection; invasive disease; chronic otitis media;
KW hearing loss; antibacterial drug.
XX
OS Moraxella catarrhalis.
XX
PN M0200015802-A1.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-EP06781.
XX
PR 14-SEP-1998; 98GB-0020002.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Ruelle J;
XX
DR WPI: 2000-271440/23.
DR N-PSDB: AAA10701.
XX
PT Novel BASB034 polynucleotides and polypeptides from Moraxella
PT catarrhalis used to prepare vaccines against bacterial infections -
XX
PS Claim 3; Page 67; 106pp; English.
XX
XX
CC This sequence represents a Moraxella catarrhalis BASB034 polypeptide from
CC strain Mc2908. The invention relates to BASB034 polypeptides from
CC M. catarrhalis strains Mc2931, Mc2908, Mc2913 and Mc2969. The BASB034
CC polynucleotides and polypeptides may be employed as research reagents and
CC material for the discovery of treatments and diagnostics for diseases,
CC particularly human diseases. They are particularly used to diagnose and
CC treat M. catarrhalis infections. They can be used for diagnosis of
CC disease, staging of disease, or determining response of an infectious
CC organism to drugs. The polynucleotides may be used as a source for
CC hybridization probes, and for screening of genetic mutations, serotype,
CC organism or strain identification, identification of mutations in BASB034
CC sequences, and as components of arrays which are useful for diagnostic
CC and prognostic purposes. The polypeptides can be used to produce
CC antibodies. The polypeptides can also be used in vaccine formulations,
CC and to identify agonists and antagonists. The polypeptides, antibodies,
CC agonists and antagonists (which are bacteriostatic) are used for the
CC treatment and prevention of diseases such as otitis media in infants and
CC children, pneumonia in elderlies, sinusitis, nosocomial infections and
CC invasive diseases, and chronic otitis media with hearing loss. The
CC polypeptides, agonists and antagonists are also used for screening of
CC antibacterial drugs. The BASB034 products of the invention can be used
CC screen for new antibacterial compounds that may target resistant
CC bacteria.
XX
SQ Sequence 442 AA;
XX
Query Match 88.2%; Score 390; DB 21; Length 442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 53 VQASQTASSTYANPLDEHEPELYTALLENKTMILNCSALNODIMRLACYDTLVHGETPA 112
DB 53 VQASQTASSTYANPLDEHEPELYTALLENKTMILNCSALNODIMRLACYDTLVHGETPA 112
QY 113 VIKTKRSIRLDETTIMQTIKGRQVYVYQETTDPIFLMGNEKGMILTKKDAKOLEYAAKQFTP 172
DB 113 VIKTKRSIRLDETTIMQTIKGRQVYVYQETTDPIFLMGNEKGMILTKKDAKOLEYAAKQFTP 172
QY 173 LLSFDDLRNNTPLMSSRPNNPMYVLPITFMHGKPNRSPPTPSHEARQFTPNRPAPELKF 232
DB 173 LLSFDDLRNNTPLMSSRPNNPMYVLPITFMHGKPNRSPPTPSHEARQFTPNRPAPELKF 232

QY 233 QVSVKAAEDLMCTSDLMFGYQOSHMOLENGKNSPPFVHDYQPEIFLTPQVYSDLP 292
 |||||||
 Db 233 QVSVKAAEDLMCTSDLMFGYQOSHMOLENGKNSPPFVHDYQPEIFLTPQVYSDLP 292
 QY 293 WDCKVRMIGMGAHVHNSGESAKLSRSNNRAYLMAGMEMKNTLVPRIMGRIFKEGSGSOP 352
 |||||||
 Db 293 WDCKVRMIGMGAHVHNSGESAKLSRSNNRAYLMAGMEMKNTLVPRIMGRIFKEGSGSOP 352
 QY 353 DDNDIIDLHYGYGVRFYLOLEKNSNLSGYRYRPRSGKALQLDYYPPLGKISGYFOI 412
 |||||||
 Db 353 DDNDIIDLHYGYGVRFYLOLEKNSNLSGYRYRPRSGKALQLDYYPPLGKISGYFOI 412
 QY 413 FQGYGSLIDYNHEATSFVGMLNDMNGL 442
 |||||||
 Db 413 FQGYGSLIDYNHEATSFVGMLNDMNGL 442

RESULT 3
 AAY85271
 ID AAY85271 standard; Protein: 442 AA.
 XX
 AC AAY85271:
 XX
 DT 29-JUN-2000 (first entry)
 XX
 DE BASB034 amino acid sequence #4.
 XX
 KM Moraxella catarrhalis infection; BASB034; diagnosis; staging;
 KM vaccine; bacteriostatic; treatment; prevention; otitis media; pneumonia;
 KM sinusitis; nosocomial infection; invasive disease; chronic otitis media;
 KM hearing loss; antibacterial drug.
 XX
 OS Moraxella catarrhalis.
 XX
 PN W0200015802-A1.
 XX
 PD 23-MAR-2000.
 XX
 PF 14-SEP-1999; 99WO-EP06781.
 XX
 PR 14-SEP-1999; 98GB-0020002.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Ruelle J;
 XX
 DR WPI; 2000-271440/23.
 DR N-PSDB; AAA10703.
 XX
 PT Novel BASB034 polynucleotides and polypeptides from Moraxella
 PT catarrhalis used to prepare vaccines against bacterial infections
 XX
 PS Claim 3; Page 69; 106pp; English.
 XX
 CC This sequence represents a Moraxella catarrhalis BASB034 polypeptide from
 CC strain Mc2969. The invention relates to BASB034 polypeptides from
 CC M. catarrhalis strains Mc2931, Mc2908, Mc2913 and Mc2969. The BASB034
 CC polynucleotides and polypeptides may be employed as research reagents and
 CC material for the discovery of treatments and diagnostics for diseases,
 CC particularly human diseases. They are particularly used to diagnose and
 CC treat M. catarrhalis infections. They can be used for diagnosis of
 CC disease, staging of disease, or determining response of an infectious
 CC organism to drugs. The polynucleotides may be used as a source for
 CC hybridization probes, and for screening of genetic mutations, serotype,
 CC organism or strain identification, identification of mutations in BASB034
 CC sequences, and as components of arrays which are useful for diagnostic
 CC and prognostic purposes. The polypeptides can be used to produce
 CC antibodies. The polypeptides can also be used in vaccine formulations,
 CC and to identify agonists and antagonists. The polypeptides, antibodies,
 CC agonists and antagonists (which are bacteriostatic) are used for the
 CC treatment and prevention of diseases such as otitis media in infants and
 CC children, pneumonia in elderlies, sinusitis, nosocomial infections and
 CC invasive diseases, and chronic otitis media with hearing loss. The

CC polypeptides, agonists and antagonists are also used for screening of
 CC antibacterial drugs. The BASB034 products of the invention can be used
 CC screen for new antibacterial compounds that may target resistant
 CC bacteria.
 CC
 XX Sequence 442 AA;
 SO
 Query Match 71.5%; Score 316; DB 21; Length 442;
 Best Local Similarity 99.8%; Pred. No. 2,2e-298;
 Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 AVPNPVAFVDEVRSENDLGQDNELPIDQASQTQASTDTANPLDEHEPELYTTALEKNTM 85
 |||||||
 Db 26 AVPNPVAFVDEVRSENDLGQDNELPIDQASQTQASTDTANPLDEHEPELYTTALEKNTM 85
 QY 86 LINCASALNODIMRLACTDTLVHGETPAVYKTKRSIRLDETWTQITKGPQVYQETTDPI 145
 |||||||
 Db 86 LINCASALNODIMRLACTDTLVHGETPAVYKTKRSIRLDETWTQITKGPQVYQETTDPI 145
 QY 146 FLMGNEKGLTKKDAKOLEYAAKQFTPLSLSFDDLRNNTPLMSSRPHNPVVLPIFMHGK 205
 |||||||
 Db 146 FLMGNEKGLTKKDAKOLEYAAKQFTPLSLSFDDLRNNTPLMSSRPHNPVVLPIFMHGK 205
 QY 206 PNRSPNTPSHBARQFTPEFRAPELKEQVSVKAAEDLMCTSDLMFGYQOSHMOLEFN 265
 |||||||
 Db 206 PNRSPNTPSHBARQFTPEFRAPELKEQVSVKAAEDLMCTSDLMFGYQOSHMOLEFN 265
 QY 266 GKNSRPFVRVHDYQPEIFLTPQVYSDLPWDGKVRMIGMGAHVHNSGESAKLSRSNNRAYLM 325
 |||||||
 Db 266 GKNSRPFVRVHDYQPEIFLTPQVYSDLPWDGKVRMIGMGAHVHNSGESAKLSRSNNRAYLM 325
 QY 326 AGMEMKNTLVMPRIMGRIFKEGSGSOPDNDIIDLHYGYGVRFYLOLEKNSNLSGYRY 385
 |||||||
 Db 326 AGMEMKNTLVMPRIMGRIFKEGSGSOPDNDIIDLHYGYGVRFYLOLEKNSNLSGYRY 385
 QY 386 NPSRGKALQLDYYPPLGKISGYFOIFQGYGOSLIDYNHEATSFVGMLNDMNGL 442
 |||||||
 Db 386 NPSRGKALQLDYYPPLGKISGYFOIFQGYGOSLIDYNHEATSFVGMLNDMNGL 442

RESULT 4
 AAO17569
 ID AAO17569 standard; Protein: 289 AA.
 XX
 AC AAO17569;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE M catarrhalis MCA100712 protein SEQ ID NO: 18.
 XX
 KM Moraxella; vaccine; respiratory tract infection; antiinflammatory;
 KM auditory; antibacterial; otitis media; sinusitis; pneumonia.
 XX
 OS Moraxella catarrhalis.
 XX
 PN W0200218595-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 28-AUG-2001; 2001WO-CA01221.
 XX
 PR 28-AUG-2000; 2000US-228294P.
 PR 28-AUG-2000; 2000US-228295P.
 PR 28-AUG-2000; 2000US-228296P.
 PR 29-AUG-2000; 2000US-228438P.
 PR 29-AUG-2000; 2000US-228439P.
 PR 29-AUG-2000; 2000US-228440P.
 PR 29-AUG-2000; 2000US-228441P.
 PR 29-AUG-2000; 2000US-228442P.
 PR 29-AUG-2000; 2000US-228443P.
 PR 29-AUG-2000; 2000US-228511P.
 PR 29-AUG-2000; 2000US-228512P.
 PR 29-AUG-2000; 2000US-228742P.

PR 29-AUG-2000; 2000US-228773P.
PR 01-SEP-2000; 2000US-229465P.
PR 01-SEP-2000; 2000US-229474P.
PR 01-SEP-2000; 2000US-229475P.
PR 01-SEP-2000; 2000US-229478P.
PR 05-SEP-2000; 2000US-229740P.
PR 05-SEP-2000; 2000US-229803P.
PR 05-SEP-2000; 2000US-229804P.
PR 05-SEP-2000; 2000US-229805P.
PR 05-SEP-2000; 2000US-229806P.
PR 05-SEP-2000; 2000US-229809P.
PR 05-SEP-2000; 2000US-229811P.
PR 06-SEP-2000; 2000US-230214P.
PR 06-SEP-2000; 2000US-230250P.
PR 06-SEP-2000; 2000US-230252P.
XX (AVER) AVENTIS PASTEUR LTD.
XX
XX
XX Loosmore S, Wang J, Bradley B, Ochs M, Yang Y;
XX
XX WPI; 2002-401721/43.
XX N-PSDB; AAL46501.
XX
XX Moraxella polypeptide and polynucleotides useful as vaccine for
PT immunizing a host e.g. humans against disease e.g. otitis media,
PT pneumonia, caused by infection of the bacteria
XX
XX Claim 26; Fig 17; 277pp; English.
XX
XX The present invention provides the protein and coding sequences of
CC proteins from Moraxella catarrhalis. These can be used to produce
CC vaccines which protect against M. catarrhalis infection, which can cause
CC otitis media, respiratory infection, sinusitis, and pneumonia. The
CC present sequence is a protein of the invention.
XX
XX Sequence 289 AA:
SO
Query Match 50.7%; Score 224; DB 23; Length 289;
Best Local Similarity 100.0%; Pred. No. 3.9e-209;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 219 QFTPNFRAPBLKQVSVKKAEDLWGTDSDLMFGYTOOSHMOIFNGKSRPRRHNDYQ 278
DB 66 QFTPNFRAPBLKQVSVKKAEDLWGTDSDLMFGYTOOSHMOIFNGKSRPRRHNDYQ 125
QY 279 PEIPLTQPVYSDDLPMWQKVMIGKAVHNSNGESAKLSRSMNRAYLMAKEMKRLTYMPR 338
DB 126 PEIPLTQPVYSDDLPMWQKVMIGKAVHNSNGESAKLSRSMNRAYLMAKEMKRLTYMPR 185
QY 339 IWGRIFKFGSGSQPDDNDPDLIDYGYDVRFLYOLEKKSNSIGTVRYNPRSGKALQLDY 398
DB 186 IWGRIFKFGSGSQPDDNDPDLIDYGYDVRFLYOLEKKSNSIGTVRYNPRSGKALQLDY 245
QY 399 VYPLGKISGYFOIFOGYGSLLIDYNEATSFVGGLMLNDMMGL 442
DB 246 VYPLGKISGYFOIFOGYGSLLIDYNEATSFVGGLMLNDMMGL 289
RESULT 5
AAY85268
ID AAY85268 standard; Protein; 442 AA.
XX
XX AAY85268;
XX
XX 29-JUN-2000 (first entry)
XX
XX BASB034 amino acid sequence #1.
XX
XX Moraxella catarrhalis infection; BASB034; diagnosis; staging;
KW vaccine; bacteriostatic; treatment; prevention; otitis media; pneumonia;
KW sinusitis; nosocomial infection; invasive disease; chronic otitis media;
KW hearing loss; antibacterial drug.
XX

OS Moraxella catarrhalis.
XX
XX W0200015802-A1.
XX
XX 23-MAR-2000.
XX
XX 14-SEP-1999; 99WO-EP06781.
XX
XX 14-SEP-1998; 98GB-0020002.
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Ruelle J;
XX
XX WPI; 2000-271440/23.
XX N-PSDB; AAL10700.
XX
XX Novel BASB034 polynucleotides and polypeptides from Moraxella
PT catarrhalis used to prepare vaccines against bacterial infections
XX
XX
XX Claim 3; Fig 2; 106pp; English.
XX
XX This sequence represents a Moraxella catarrhalis BASB034 polypeptide from
CC strain Mc2931 (ATCC 43617). The invention relates to BASB034 polypeptides
CC from M. catarrhalis strains Mc2931, Mc2908, Mc2913 and Mc2969. The
CC BASB034 polynucleotides and polypeptides may be employed as research
CC reagents and material for the discovery of treatments and diagnostics for
CC diseases, particularly human diseases. They are particularly used to
CC diagnose and treat M. catarrhalis infections. They can be used for
CC diagnosis of disease, staging of disease, or determining response of an
CC infectious organism to drugs. The polynucleotides may be used as a source
CC for hybridization probes, and for screening of genetic mutations,
CC serotype, organism or strain identification, identification of mutations
CC in BASB034 sequences, and as components of arrays which are useful for
CC diagnostic and prognostic purposes. The polypeptides can be used to
CC produce antibodies. The polypeptides can also be used in vaccine
CC formulations, and to identify agonists and antagonists. The polypeptides,
CC antibodies, agonists and antagonists (which are bacteriostatic) are used
CC for the treatment and prevention of diseases such as otitis media in
CC infants and children, pneumonia in elderly, sinusitis, nosocomial
CC infections and invasive diseases, and chronic otitis media with hearing
CC loss. The polypeptides, agonists and antagonists are also used for
CC screening of antibacterial drugs. The BASB034 products of the invention
CC can be used screen for new antibacterial compounds that may target
CC resistant bacteria.
XX
XX Sequence 442 AA:
SO
Query Match 50.7%; Score 224; DB 21; Length 442;
Best Local Similarity 100.0%; Pred. No. 5.6e-209;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 219 QFTPNFRAPBLKQVSVKKAEDLWGTDSDLMFGYTOOSHMOIFNGKSRPRRHNDYQ 278
DB 219 QFTPNFRAPBLKQVSVKKAEDLWGTDSDLMFGYTOOSHMOIFNGKSRPRRHNDYQ 278
QY 279 PEIPLTQPVYSDDLPMWQKVMIGKAVHNSNGESAKLSRSMNRAYLMAKEMKRLTYMPR 338
DB 279 PEIPLTQPVYSDDLPMWQKVMIGKAVHNSNGESAKLSRSMNRAYLMAKEMKRLTYMPR 338
QY 339 IWGRIFKFGSGSQPDDNDPDLIDYGYDVRFLYOLEKKSNSIGTVRYNPRSGKALQLDY 398
DB 339 IWGRIFKFGSGSQPDDNDPDLIDYGYDVRFLYOLEKKSNSIGTVRYNPRSGKALQLDY 398
QY 399 VYPLGKISGYFOIFOGYGSLLIDYNEATSFVGGLMLNDMMGL 442
DB 399 VYPLGKISGYFOIFOGYGSLLIDYNEATSFVGGLMLNDMMGL 442
RESULT 6
ABG18034
ID ABG18034 standard; Protein; 255 AA.
XX

AC ABG18034;
 XX
 DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #18025.
 DE
 XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS82221.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20: SEQ ID No 48393; 103pp: English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations in
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 255 AA;
 Query Match 2.0%; Score 9; DB 22; Length 255;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 279 PEIFLTQPV 287
 DB 204 PEIFLTQPV 212

DT 21-MAR-2000 (first entry)
 XX
 DE Neisseria gonorrhoeae ORF 582 protein sequence SEQ ID NO:1786.
 XX
 XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 KM antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
 KM antibacterial; gene therapy.
 XX
 OS Neisseria gonorrhoeae.
 XX
 PN WO957280-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-US09346.
 XX
 PR 01-MAY-1998; 98US-0083758.
 PR 31-JUL-1998; 98US-0094869.
 PR 02-SEP-1998; 98US-0098994.
 PR 02-SEP-1998; 98US-0099062.
 PR 09-OCT-1998; 98US-0103749.
 PR 09-OCT-1998; 98US-0103794.
 PR 09-OCT-1998; 98US-0103796.
 PR 25-FEB-1999; 99US-0121528.
 XX
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;
 PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
 PI Tettelin H, Venter JC;
 XX
 DR WPI; 2000-062150/05.
 DR N-PSDB; AAZ53918.
 XX
 PT Novel Neisserial polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics -
 XX
 PS Claim 2; Page 903; 1453pp: English.
 XX
 CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
 CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of
 CC the invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the
 CC manufacture of medicaments for treating or preventing infection due to
 CC Neisserial bacteria (e.g. meningitis and septicemia), to detect the
 CC presence of Neisseria bacteria, or to raise antibodies. They may also
 CC be used to screen for agonists or antagonists, which may themselves
 CC have use as antibacterial agents. The polynucleotides of the invention
 CC may also be used in gene therapy protocols.
 XX
 SQ Sequence 370 AA;
 Query Match 2.0%; Score 9; DB 21; Length 370;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 279 PEIFLTQPV 287
 DB 209 PEIFLTQPV 217

RESULT 7
 AAY75156
 ID AAY75156 standard; Protein; 370 AA.
 XX
 AC AAY75156;
 XX

RESULT 8
 AAY75157
 ID AAY75157 standard; Protein; 370 AA.
 XX
 AC AAY75157;
 XX
 DT 21-MAR-2000 (first entry)
 XX

DE		Neisseria meningitidis ORF 582 protein sequence SEQ ID NO:1788.
xx		
KW		Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KM		antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KW		antibacterial; gene therapy.
xx		
OS		Neisseria meningitidis .
XX		
PN		W09957280-A2.
XX		
PD		11-NOV-1999.
XX		
PF		30-APR-1999; 99WO-US09346.
XX		
PR		01-MAY-1998; 98US-0083758.
PR		31-JUL-1998; 98US-0094869.
PR		02-SEP-1998; 98US-0098994.
PR		02-SEP-1998; 98US-0099062.
PR		09-OCT-1998; 98US-0103749.
PR		09-OCT-1998; 98US-0103794.
PR		09-OCT-1998; 98US-0103796.
PR		25-FEB-1999; 99US-0121528.
XX		
PA		(CHIR) CHIRON CORP.
PA		(GENO) INST GENOMIC RES.
XX		
P1		Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;
P1		Peteresen J, Pizsa M, Rappucci R, Ratti G, Scalato E, Scarselli M;
P1		Tetteijn H, Venter JC;
XX		
DR		WPI: 2000-062150/05.
DR		N-PDB: AAZ53919.
XX		
PT		Novel Neisserial polypeptides predicted to be useful antigens for
PT		vaccines and diagnostics -
xx		
PS		Claim 2; Page 904; 1453pp; English.
XX		
CC		AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC		represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC		and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent
CC		PCR primers used in the exemplification of the present invention. The
CC		polypeptides, the polynucleotides, antibodies and compositions of
CC		the invention can be used as vaccines, as diagnostic reagents, and as
CC		immunogenic compositions. The polypeptides can be used in the
CC		manufacture of medicaments for treating or preventing infection due to
CC		Neisserial bacteria (e.g. meningitis and septicæmia), to detect the
CC		presence of Neisseria bacteria, or to raise antibodies. They may also
CC		be used to screen for agonists or antagonists, which may themselves
CC		have use as antibacterial agents. The polynucleotides of the invention
CC		may also be used in gene therapy protocols.
xx		
SQ		Sequence 370 AA:
Yy		
Query Match	2.0%; Score 9; DB 21; Length 370;	
Best Local Similarity	100.0%; Pred. No. 4;	
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db		
Oy	279 PEIPLTOPV 287	
	PEIPLTOPV 217	
RESULT 9		
AAZ75158		
ID	AAZ75158 standard; Protein: 370 AA.	
XX		
AC	AAZ75158;	
XX		
DT	21-MAR-2000 (first entry)	
XX		
DE	Neisseria meningitidis ORF 582 protein sequence SEQ ID NO:1790.	

KM	Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW	antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KV	antibacterial; gene therapy.
XX	
OS	Neisseria meningitidis.
XX	
PN	W0957280-A2.
XX	
PD	11-NOV-1999.
XX	
XX	30-APR-1999; 99WO-US09346.
PF	
XX	01-MAY-1998; 98US-0083758.
PR	31-JUL-1998; 98US-0094869.
PR	02-SEP-1998; 98US-0098994.
PR	02-SEP-1998; 98US-0099062.
PR	09-OCT-1998; 98US-0103749.
PR	09-OCT-1998; 98US-0103794.
PR	09-OCT-1998; 98US-0103796.
PR	25-FEB-1999; 99US-0121528.
XX	
PA	(CHIR) CHIRON CORP.
PA	(GENO-) INST GENOMIC RES.
XX	
PI	Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI	Peteren J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI	Tettelin H, Venter JC;
XX	
XX	WPI: 2000-062150/05.
DR	N-PSDB: AA253920.
XX	
PT	Novel Neisserial polypeptides predicted to be useful antigens for
PT	vaccines and diagnostics
XX	
PS	Claim 2: Page 905: 1453pp; English.
XX	
CC	AA253015 to AA254536, AA254577 to AA254615, and AA74253 to AA75941
CC	represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC	and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent
CC	PCR primers used in the exemplification of the present invention. The
CC	polypeptides, the polynucleotides, antibodies and compositions of
CC	the invention can be used as vaccines, as diagnostic reagents, and as
CC	immunogenic compositions. The polypeptides can be used in the
CC	manufacture of medicaments for treating or preventing infection due to
CC	Neisserial bacteria (e.g. meningitis and septicaemia), to detect the
CC	presence of Neisseria bacteria, or to raise antibodies. They may also
CC	be used to screen for agonists or antagonists, which may themselves
CC	have use as antibacterial agents. The polynucleotides of the invention
XX	may also be used in gene therapy protocols.
XX	
SO	Sequence 370 AA;
XX	
Query Match	2.0%; Score 9; DB 21; Length 370;
Best Local Similarity	100.0%; Pred. No. 4;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	279 PEIFLTPV 287
DB	209 PEIFLTPV 217
IIIIIIIIII	
RESULT 10	
AA770629	
ID	AA770629 standard; Protein; 374 AA.
XX	
AC	AA770629;
XX	
DT	18-JUL-2000 (first entry)
XX	
DE	Neisseria meningitidis serogroup B strain H44/76 BASB033 protein.
XX	
KW	BASB033; diagnosis; prophylaxis; treatment; antibacterial; vaccine;
KV	Neisseria meningitidis infection.

XX OS Neisseria meningitidis.
XX PN WO200015801-A1.
XX PD 23-MAR-2000.
XX PF 09-SEP-1999; 99WO-EP06718.
XX PR 14-SEP-1998; 98GB-0020003.
XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Ruelle J;
XX DR WPI; 2000-271439/23.
XX DR N-PSDB; AA252134.
XX PT Isolated BASB033 polypeptides and polynucleotides of Neisseria
XX PT meningitidis, useful for diagnosis, prophylaxis and treatment of N.
XX PS meningitidis infection -
XX PS Claim 4; Page 59; 93pp; English.
XX CC The present sequence is a BASB033 protein from
XX CC Neisseria meningitidis serogroup B strain H44/76. The protein
XX CC shows homology to the Klebsiella pneumoniae outer membrane
XX CC phospholipase A. The present sequence is useful for diagnosis,
XX CC prophylaxis and treatment of N. meningitidis infection. It may also be
XX CC used for the discovery and development of antibacterial compounds and
XX CC in vaccine compositions.
XX SQ Sequence 374 AA;
OY 279 PEIFLTQPV 287
DB 213 PEIFLTQPV 221

Query Match 2.0%; Score 9; DB 21; Length 374;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
ID AAY70628 standard; Protein; 375 AA.
XX AC AAY70628;
XX DT 18-JUL-2000 (first entry)
XX DE Neisseria meningitidis serogroup B strain ATCC13090 BASB033 protein.
XX KM BASB033; diagnosis, prophylaxis; treatment; antibacterial; vaccine;
XX KM Neisseria meningitidis infection.
XX OS Neisseria meningitidis.
XX PN WO200015801-A1.
XX PD 23-MAR-2000.
XX PF 09-SEP-1999; 99WO-EP06718.
XX PR 14-SEP-1998; 98GB-0020003.
XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Ruelle J;
XX DR WPI; 2000-271439/23.
XX DR N-PSDB; AA252133.

PT Isolated BASB033 polypeptides and polynucleotides of Neisseria
PT meningitidis, useful for diagnosis, prophylaxis and treatment of N.
PT meningitidis infection -
XX PS Claim 4; Page 58; 93pp; English.
XX CC The present sequence is a BASB033 protein from
XX CC Neisseria meningitidis serogroup B strain ATCC13090. The protein
XX CC shows homology to the Klebsiella pneumoniae outer membrane
XX CC phospholipase A. The present sequence is useful for diagnosis,
XX CC prophylaxis and treatment of N. meningitidis infection. It may also be
XX CC used for the discovery and development of antibacterial compounds and
XX CC in vaccine compositions.
XX SQ Sequence 375 AA;
OY 279 PEIFLTQPV 287
DB 214 PEIFLTQPV 222

Query Match 2.0%; Score 9; DB 21; Length 375;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
ID AAG1137 standard; Protein; 278 AA.
XX AC AAG1137;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 9741.
XX KM Protein identification; signal transduction pathway; metabolic pathway;
XX KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX KM termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
XX PR 29-MAR-1999; 99US-0126785.
XX PR 01-APR-1999; 99US-0127462.
XX PR 06-APR-1999; 99US-0128234.
XX PR 08-APR-1999; 99US-0128714.
XX PR 16-APR-1999; 99US-0129845.
XX PR 19-APR-1999; 99US-0130077.
XX PR 21-APR-1999; 99US-0130449.
XX PR 23-APR-1999; 99US-0130510.
XX PR 23-APR-1999; 99US-0130891.
XX PR 28-APR-1999; 99US-0131449.
XX PR 30-APR-1999; 99US-0132048.
XX PR 30-APR-1999; 99US-0132407.
XX PR 04-MAY-1999; 99US-0132484.
XX PR 05-MAY-1999; 99US-0132485.
XX PR 06-MAY-1999; 99US-0132486.
XX PR 06-MAY-1999; 99US-0132487.
XX PR 07-MAY-1999; 99US-0132863.
XX PR 11-MAY-1999; 99US-0134256.
XX PR 14-MAY-1999; 99US-0134218.
XX PR 14-MAY-1999; 99US-0134219.
XX PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 03-JUN-1999; 99US-0137222.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139494.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0144816.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145214.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0153486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156559.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.

PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 1.8%; Score 8; DB 21; Length 278;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 174 SLSPDLR 181
Db 271 SLSPDLR 278
|||||

RESULT 13
AAAG1136
ID AAAG1136 standard; Protein; 283 AA.
XX
AC AAAG1136;
XX
DI 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9740.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.
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DF 17-OCT-2000 (first entry)
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KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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PN EP1033405-A2.
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PD 06-SEP-2000.
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Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 174 SLSPDR 181

Db 292 SLSEDLDR 299

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RESULT 15

AAR52127 AAR52127 standard; Peptide; 16 AA.

XX AAR52127;

AC AAR52127; (first entry)

DT 27-SEP-1996 (first entry)

XX Mouse light chain surface patch S03410.

XX antibody: humanised; murine; human; heavy chain; light; variable;

KW framework region; complementarity determining region; reshaping;

KW modelling; surface residue; modify.

XX Mus sp.

OS EP592106-A1.

PN 13-APR-1994.

PD 07-SEP-1993; 93EP-0307051.

XX 09-SEP-1992; 92US-0942245.

PR (PEDE/) PEDERSEN J T.

XX (IMM-) IMMUNOGEN INC.

PA Guld BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;

PI WPI; 1994-120230/15.

DR Method of resurfacing of rodent antibodies to produce humanised

XX antibody forms - for producing non-human antibodies with improved

PT therapeutic efficiency by presenting human surface on V-region

PS Example 1; Page 14; 230pp; English.

XX Modification of a rodent antibody or fragment by resurfacing in order

CC to produce a humanised rodent antibody can be determined by calculating

CC homology between murine and human antibody surfaces. In order to test

CC the resurfacing approach of the invention, three humanisation

CC experiments were set up. (1) traditional loop grafting; (2) resurfacing

CC approach using most similar chain; and (3) resurfacing approach using

CC human sequences with most similar surface residues. AAR52069-159 are the

CC surface residue patterns in mouse light chain antibody variable regions.

CC These "patches" were used in the third method, where rodent light and

CC heavy chains were matched and the most similar human sequence found

CC independently only over the surface residues indicated in AAR52030-67.

XX

SO Sequence 16 AA;

Query Match 1.6%; Score 7; DB 15; Length 16;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 387 PRSGKGA 393

Db 4 PRSGKGA 10

Search completed: November 12, 2002, 11:44:52
Job time : 31 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:46 : Search time 11 Seconds
(without alignments)
1182.267 Million cell updates/sec

Title: US-09-787-083-6
Perfect score: 442
Sequence: 1 MKYSLSTLSTLSCEFAILA.....YNHEATSPFGVGLNDWMGL 442

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCFUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	1.6	16	1	US-07-942-245-98 Sequence 98, Appl
2	7	1.6	347	4	US-09-097-889-14 Sequence 14, Appl
3	7	1.6	552	1	US-08-231-729B-6 Sequence 6, Appl
4	7	1.6	900	4	US-08-890-865A-4 Sequence 4, Appl
5	7	1.6	934	1	US-08-215-805A-80 Sequence 80, Appl
6	7	1.6	1026	2	US-08-342-003-6 Sequence 6, Appl
7	7	1.6	1026	2	US-08-342-003-6 Sequence 6, Appl
8	7	1.6	1026	2	US-08-342-003-6 Sequence 6, Appl
9	6	1.4	10	3	US-08-974-775-30 Sequence 30, Appl
10	6	1.4	11	3	US-08-974-775-29 Sequence 29, Appl
11	6	1.4	12	3	US-08-974-775-28 Sequence 28, Appl
12	6	1.4	13	3	US-08-974-775-8 Sequence 8, Appl
13	6	1.4	13	3	US-08-974-775-27 Sequence 27, Appl
14	6	1.4	14	3	US-08-974-775-9 Sequence 9, Appl
15	6	1.4	14	3	US-08-974-775-10 Sequence 10, Appl
16	6	1.4	14	3	US-08-974-775-32 Sequence 32, Appl
17	6	1.4	15	3	US-08-974-775-5 Sequence 5, Appl
18	6	1.4	16	3	US-08-974-775-4 Sequence 4, Appl
19	6	1.4	20	1	US-08-430-273-1 Sequence 1, Appl
20	6	1.4	21	1	US-07-918-953-13 Sequence 13, Appl
21	6	1.4	21	1	US-07-918-953-15 Sequence 15, Appl
22	6	1.4	21	1	US-08-212-696-1 Sequence 1, Appl
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24	6	1.4	21	1	US-08-081-661-13 Sequence 13, Appl
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37	6	1.4	21	2	US-08-508-664-9 Sequence 9, Appl
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ALIGNMENTS

RESULT 1
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Sequence 98, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROCUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ. ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-98

Query Match 1.6%; Score 7; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 PRSGGA 393
|||||
Db 4 PRSGGA 10

RESULT 2
US-09-097-889-14
Sequence 14, Application US/09097889
Patent No. 6218117
GENERAL INFORMATION:
APPLICANT: Heinstadt, Corinna
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
TITLE OF INVENTION: AGENTS THAT QUANTITATIVELY ALTER DETECTABLE
TITLE OF INVENTION: EXPRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,889
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.417
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-097-889-14
Query Match 1.6%; Score 7; DB 4; Length 347;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 LRTSLS 14
DB 155 LRTSLS 161
RESULT 3
US-08-231-729B-6
Sequence 6, Application US/08231729B
Patent No. 5618722
GENERAL INFORMATION:
APPLICANT: ZENNO, Shuhei
APPLICANT: SHIRATSU, Shinji
APPLICANT: INOUE, Satoshi
APPLICANT: SAIGO, Kaoru
TITLE OF INVENTION: FIREFLY LUCIFERASE GENE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER
STREET: 700 Thirteenth Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,729B
FILING DATE: 20-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 119050/1993
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rose, Herbert C.
REGISTRATION NUMBER: 29846
REFERENCE/DOCKET NUMBER: 60130/No. 5618722aka
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-6770
TELEFAX: 202-737-6776
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-231-729B-6
Query Match 1.6%; Score 7; DB 1; Length 552;
Best Local Similarity 100.0%; Pred. No. 1,3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 175 LSFPLDR 181
DB 184 LSFPLDR 190
RESULT 4
US-08-890-865A-4
Sequence 4, Application US/08890865A
Patent No. 6307019
GENERAL INFORMATION:
APPLICANT: Constantini, Franklin
APPLICANT: Zeng, Li
TITLE OF INVENTION: AXIN GENE AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,865A
FILING DATE: 10-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/54249
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-890-865A-4

Query Match 1.6%; Score 7; DB 4; Length 900;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 403 GKGISGY 409
Db 268 GKGISGY 274

RESULT 5
US-08-215-805A-80
Sequence 80, Application US/08215805A
Patent No. 5559008
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: LEUKOCOXIN GENE FROM PASTEURILLA
TITLE OF INVENTION: SUIS
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,805A
FILING DATE: 22-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timlan, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 934 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Pasteurella suis
STRAIN: 5943
IMMEDIATE SOURCE:
LIBRARY: P. suis DNA in Bacteriophage lambda-dash
CLONE: (Lambda)yfc33-37
US-08-215-805A-80

Query Match 1.6%; Score 7; DB 1; Length 934;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 238 VKAADL 244
Db 62 VKAADL 68

RESULT 6
US-08-542-003-6
Sequence 6, Application US/08542003
Patent No. 5864013
GENERAL INFORMATION:
APPLICANT: Goldberg, Edward B.
TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF

TITLE OF INVENTION: NANOMETER STRUCTURES AND USE THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,003
FILING DATE: 13-OCT-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8471-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: 212-869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacteriophage T4
IMMEDIATE SOURCE:
CLONE: p37 amino acid
US-08-542-003-6

Query Match 1.6%; Score 7; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 128 QTIKGP 134
Db 861 QTIKGP 867

RESULT 7
US-08-322-760A-6
Sequence 6, Application US/08322760A
Patent No. 5877279
GENERAL INFORMATION:
APPLICANT: Goldberg, Edward B.
TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF
TITLE OF INVENTION: NANOMETER STRUCTURES AND USE THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,760A
FILING DATE: 13-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:

NAME: Mierock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8471-0003-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: 212-869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacteriophage T4
IMMEDIATE SOURCE:
CLONE: p37 amino acid
US-08-322-760A-6

Query Match 1.6%; Score 7; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 QTIRGKP 134
|||||
Db 861 QTIRGKP 867

RESULT 8
US-09-236-949-6
Sequence 6, Application US/09236949
Patent No. 6437112
GENERAL INFORMATION:
APPLICANT: Goldberg, Edward B.
TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,949
FILING DATE: 25-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/542,003
FILING DATE: 13-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mierock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8471-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: 212-869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacteriophage T4
IMMEDIATE SOURCE:

CLONE: p37 amino acid
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-236-949-6

Query Match 1.6%; Score 7; DB 4; Length 1026;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 QTIRGKP 134
|||||
Db 861 QTIRGKP 867

RESULT 9
US-08-974-775-30
Sequence 30, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-30

Query Match 1.4%; Score 6; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 424 NHEATS 429
|||||
Db 5 NHEATS 10

RESULT 10
US-08-974-775-29
Sequence 29, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES

TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-29

Query Match 1.4%; Score 6; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
|||||
DB 5 NHEATS 10

RESULT 11
US-08-974-775-28
Sequence 28, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.

REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-28

Query Match 1.4%; Score 6; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
|||||
DB 5 NHEATS 10

RESULT 12
US-08-974-775-8
Sequence 8, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-8

Query Match 1.4%; Score 6; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
|||||
DB 8 NHEATS 13

RESULT 13
US-08-974-775-27
Sequence 27, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
APPLICANT: Walsh-Reitz, Margaret
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-27
Query Match 1.4%; Score 6; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 424 NHEATS 429
DB 5 NHEATS 10

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-974-775-9
Query Match 1.4%; Score 6; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 424 NHEATS 429
DB 8 NHEATS 13
RESULT 15
US-08-974-775-10
Sequence 10, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
APPLICANT: Walsh-Reitz, Margaret
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

: MOLECULE TYPE: peptide
US-08-974-775-10

Query Match 1.48; Score 6; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 424 NHEATS 429
|||||
Db 8 NHEATS 13

Search completed: November 12, 2002, 11:49:14
Job time : 13 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:45:00 ; Search time 5.75 Seconds

(without alignments)
1108,344 Million cell updates/sec

Title: US-09-787-083-6

Perfect score: 442
Sequence: 1 MKVSLSTLTITLITSCFAAILA.....YNHEATSFVGLMINDMGL 442Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 92612 seqs, 14418503 residues

Word size : 0

Total number of hits satisfying chosen parameters: 92612

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
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7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	1.6	75	10	US-09-764-869-1013 Sequence 1013, App
2	7	1.6	347	10	US-09-098-079-14 Sequence 14, Appl
3	7	1.6	511	10	US-09-773-882-2 Sequence 2, Appl1
4	7	1.6	511	10	US-09-773-882-11 Sequence 11, Appl
5	7	1.6	513	10	US-09-815-242-11029 Sequence 11029, A
6	7	1.6	783	10	US-09-825-144-2 Sequence 4, Appl1
7	7	1.6	829	10	US-09-825-144-4 Sequence 2, Appl1
8	6	1.4	15	10	US-09-947-770-20 Sequence 20, Appl
9	6	1.4	17	10	US-09-732-561-23 Sequence 23, Appl
10	6	1.4	21	9	US-09-947-563-1 Sequence 1, Appl1
11	6	1.4	21	9	US-09-947-563-7 Sequence 7, Appl1
12	6	1.4	21	10	US-09-853-844-1 Sequence 1, Appl1
13	6	1.4	21	10	US-09-815-229-1 Sequence 102, App
14	6	1.4	22	12	US-10-066-151-102 Sequence 102, App
15	6	1.4	26	10	US-09-864-761-43426 Sequence 43426, A
16	6	1.4	28	12	US-10-014-269-9 Sequence 9, Appl1
17	6	1.4	30	10	US-09-815-229-16 Sequence 16, Appl
18	6	1.4	33	10	US-09-030-619-175 Sequence 175, App
19	6	1.4	39	10	US-09-205-658-116 Sequence 116, App

20	6	1.4	39	12	US-10-042-417-18 Sequence 18, Appl
21	6	1.4	46	10	US-09-205-658-132 Sequence 132, App
22	6	1.4	46	10	US-09-205-658-133 Sequence 133, App
23	6	1.4	46	10	US-09-205-658-136 Sequence 136, App
24	6	1.4	50	10	US-09-853-844-4 Sequence 4, Appl1
25	6	1.4	50	10	US-09-864-761-41965 Sequence 41965, A
26	6	1.4	51	9	US-10-028-410-3 Sequence 3, Appl1
27	6	1.4	54	10	US-09-815-229-13 Sequence 13, Appl
28	6	1.4	56	10	US-09-864-761-41804 Sequence 41804, A
29	6	1.4	64	10	US-09-864-761-36407 Sequence 36407, A
30	6	1.4	73	12	US-10-062-254-16 Sequence 16, Appl
31	6	1.4	78	10	US-09-864-761-38666 Sequence 38666, A
32	6	1.4	81	10	US-09-799-514-14 Sequence 14, Appl
33	6	1.4	86	9	US-09-878-380-1 Sequence 1, Appl1
34	6	1.4	86	9	US-10-028-410-2 Sequence 2, Appl1
35	6	1.4	90	10	US-09-887-586A-35 Sequence 35, Appl
36	6	1.4	90	10	US-09-903-012-35 Sequence 35, Appl
37	6	1.4	91	10	US-09-864-761-46089 Sequence 46089, A
38	6	1.4	91	10	US-09-815-242-5022 Sequence 5022, Ap
39	6	1.4	91	10	US-09-815-242-10688 Sequence 10688, A
40	6	1.4	96	9	US-09-947-563-5 Sequence 4, Appl1
41	6	1.4	96	9	US-09-947-563-5 Sequence 5, Appl1
42	6	1.4	96	12	US-10-062-254-18 Sequence 18, Appl
43	6	1.4	99	10	US-09-764-869-1082 Sequence 1082, Ap
44	6	1.4	100	10	US-09-925-301-1520 Sequence 1520, Ap
45	6	1.4	103	9	US-10-050-786-9 Sequence 9, Appl1

ALIGNMENTS

```
RESULT 1
US-09-764-869-1013
: Sequence 1013, Application US/09764869
: Patent No. US20020061521A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC007
: CURRENT APPLICATION NUMBER: US/09/764, 869
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - refer to PALM or file wrapper
: NUMBER OF SEQ ID NOS: 2442
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1013
: LENGTH: 75
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (61)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (74)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-869-1013

Query Match 1.6%; Score 7; DB 10; Length 75;
Best local similarity 100.0%; Pred. No. 6.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VSLSTLT 9
Db 44 VSLSTLT 50

RESULT 2
US-09-098-079-14
: Sequence 14, Application US/09098079
: Patent No. US20020064773A1
: GENERAL INFORMATION:
: APPLICANT: Herinstdt, Corrina
: APPLICANT: Ghosh, Soumitra S.
```

APPLICANT: Clevenger, William
APPLICANT: Fainy, Eoin F.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Roseman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.416
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-098-079-14

Query Match 1.6%; Score 7; DB 10; Length 347;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LTLSTLS 14
Db 155 LTLSTLS 161

RESULT 3
US-09-773-882-2
Sequence 2, Application US/09773882
Patent No. US20020106769A1
GENERAL INFORMATION:
APPLICANT: Omura, Mitsuo
APPLICANT: Inagaki, Tomoko
APPLICANT: Matsumoto, Ryoji
APPLICANT: Moriguchi, Takaya
APPLICANT: Hasegawa, Shin
TITLE OF INVENTION: UDP-D-Glucose:Limonoid Glucosyltransferase
FILE REFERENCE: 0119.98
CURRENT APPLICATION NUMBER: US/09/773,882
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: JP 2000-021179
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 511
TYPE: PRT
ORGANISM: Citrus unshiu
US-09-773-882-2

Query Match 1.6%; Score 7; DB 10; Length 511;
Best Local Similarity 100.0%; Pred. No. 37;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 32 AFVDEVR 38
Db 459 AFVDEVR 465

RESULT 4
US-09-773-882-11
Sequence 11, Application US/09773882
Patent No. US20020106769A1
GENERAL INFORMATION:
APPLICANT: Omura, Mitsuo
APPLICANT: Inagaki, Tomoko
APPLICANT: Matsumoto, Ryoji
APPLICANT: Moriguchi, Takaya
APPLICANT: Hasegawa, Shin
APPLICANT: Suhayda, Charles
TITLE OF INVENTION: UDP-D-Glucose:Limonoid Glucosyltransferase
FILE REFERENCE: 0119.98
CURRENT APPLICATION NUMBER: US/09/773,882
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: JP 2000-021179
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 511
TYPE: PRT
ORGANISM: Citrus unshiu
US-09-773-882-11

Query Match 1.6%; Score 7; DB 10; Length 511;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 AFVDEVR 38
Db 459 AFVDEVR 465

RESULT 5
US-09-815-242-11029
Sequence 11029, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11029
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-11029

Query Match 1.6%; Score 7; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 168 KOFTEPLS 174
DB 434 KOFTEPLS 440

RESULT 6
US-09-825-144-2
; Sequence 2, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Mathias Krause
; APPLICANT: Antonio S. Secchi
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Wehland
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 783
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-144-2

Query Match 1.6%; Score 7; DB 10; Length 783;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 268 NSRPFRV 274
DB 17 NSRPFRV 23

RESULT 7
US-09-825-144-4
; Sequence 4, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Mathias Krause
; APPLICANT: Antonio S. Secchi
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Wehland
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-144-4

Query Match 1.6%; Score 7; DB 10; Length 829;

Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 268 NSRPFRV 274
DB 17 NSRPFRV 23

RESULT 8
US-09-947-770-20
; Sequence 20, Application US/09947770
; Patent No. US20020068715A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Ruiz, Pedro
; APPLICANT: Garren, Hideki
; TITLE OF INVENTION: DNA Vaccination for Treatment of
; FILE REFERENCE: STAN123CIP
; CURRENT APPLICATION NUMBER: US/09/947,770
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/06233
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/267,590
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Insulin A (7-21) peptide
US-09-947-770-20

Query Match 1.4%; Score 6; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 LYOLEN 375
DB 7 LYOLEN 12

RESULT 9
US-09-732-561-23
; Sequence 23, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
; APPLICANT: Thoma, Bart
; APPLICANT: Terras, Franky
; APPLICANT: Pennlnckx, Iris
; APPLICANT: Manners, John
; APPLICANT: Kazan, Kemal
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Ag Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,561
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschultz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1659
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-732-561-23

Query Match 1.4%: Score 6; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 415 GYGQSL 420
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DB 11 GYGQSL 16

RESULT 10
US-09-947-563-1
Sequence 1, Application US/09947563
Patent No. US20020156234A1
GENERAL INFORMATION:
APPLICANT: Rubroder, Franz-Josef
Keller, Reinhold
TITLE OF INVENTION: Improved process for obtaining
insulin precursors having correctly bonded cysteine bridges
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farrabow, Garrett &
Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/947,563
FILING DATE: 07-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/134,836
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Leslie McDonnell
REGISTRATION NUMBER: 34,872
REFERENCE/DOCKET NUMBER: 02481.1600-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: Protein
LOCATION: 1..21
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-947-563-1

Query Match 1.4%: Score 6; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 LYOLEN 375
|||||
DB 13 LYOLEN 18

RESULT 11
US-09-947-563-7
Sequence 7, Application US/09947563
Patent No. US20020156234A1
GENERAL INFORMATION:
APPLICANT: Rubroder, Franz-Josef
Keller, Reinhold
TITLE OF INVENTION: Improved process for obtaining
insulin precursors having correctly bonded cysteine bridg
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farrabow, Garrett &
Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/947,563
FILING DATE: 07-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/134,836
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Leslie McDonnell
REGISTRATION NUMBER: 34,872
REFERENCE/DOCKET NUMBER: 02481.1600-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: Protein
LOCATION: 1..21
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-947-563-7

Query Match 1.4%: Score 6; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 LYOLEN 375
|||||
DB 13 LYOLEN 18

RESULT 12
US-09-853-844-1
; Sequence 1, Application US/09853844
; Patent No. US20020013269A1
; GENERAL INFORMATION:
; APPLICANT: Balschmidt, Per
; APPLICANT: Brange, Veligaard Jens Jorgen
; TITLE OF INVENTION: Human Insulin Analogues
; FILE REFERENCE: 3343.270-US
; CURRENT APPLICATION NUMBER: US/09/853,844
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 08/965,221
; PRIOR FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: 08/531,842
; PRIOR FILING DATE: 1995-09-21
; PRIOR APPLICATION NUMBER: 08/275,196
; PRIOR FILING DATE: 1994-07-14
; PRIOR APPLICATION NUMBER: 07/976,805
; PRIOR FILING DATE: 1992-11-16
; PRIOR APPLICATION NUMBER: 07/453,445
; PRIOR FILING DATE: 1989-12-20
; PRIOR APPLICATION NUMBER: 07/416,218
; PRIOR FILING DATE: 1989-10-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-853-844-1

Query Match 1.4%; Score 6; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 LYOLEN 375
|||||
DB 13 LYOLEN 18

RESULT 13
US-09-815-229-1
; Sequence 1, Application US/09815229
; Patent No. US20020058614A1
; GENERAL INFORMATION:
; APPLICANT: Filvaroff, Ellen H.
; APPLICANT: Okumu, Franklin W.
; TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGEOUS DISORDERS
; FILE REFERENCE: P1766RIUS
; CURRENT APPLICATION NUMBER: US/09/815,229
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/192,103
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-815-229-1

Query Match 1.4%; Score 6; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 LYOLEN 375
|||||
DB 13 LYOLEN 18

RESULT 14
US-10-066-151-102
; Sequence 102, Application US/10066151
; Patent No. US20020132300A1
; GENERAL INFORMATION:
; APPLICANT: Hogan, Patrick G.
; APPLICANT: Rao, Anjana
; APPLICANT: Aramburu, Jose
; TITLE OF INVENTION: SPECIFIC INHIBITORS OF NEAT ACTIVATION
; TITLE OF INVENTION: BY CALCINEURIN AND THEIR USE IN TREATING IMMUNE-RELATED
; FILE REFERENCE: 10861-004002
; CURRENT APPLICATION NUMBER: US/10/066,151
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 09/248,620
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/074,467
; PRIOR FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide containing the
US-10-066-151-102

Query Match 1.4%; Score 6; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 212 TPSSHEA 217
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DB 15 TPSSHEA 20

RESULT 15
US-09-864-761-43426
; Sequence 43426, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665

/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 43426
/ LENGTH: 26
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AL031587.3
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL - 1.3
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 1.8
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL - 1.2
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL - 1.7
US-09-864-761-43426

Query Match 1.4%; Score 6; DB 10; Length 26;
Best Local Similarity 100.0%; Pred.No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 345 KEGSGS 350
|||||
Db 9 KEGSGS 14

Search completed: November 12, 2002, 11:49:42
Job time : 6.75 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:45 ; Search time 13.75 Seconds
(without alignments)
3090.285 Million cell updates/sec

Title: US-09-787-083-6

Perfect score: 442

Sequence: 1 MKVSLSTLSTLSCFAILA.....YVHEATSEGVGLMDNMGL 442

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2.0	382	2	E81195	phospholipase A1,
2	2.0	409	2	H81831	probable phospholip
3	1.8	286	2	B36971	outer membrane pho
4	1.8	299	2	T47989	RAV-like protein -
5	1.8	1396	2	S36851	L-shaped tail fibre
6	1.6	68	2	B97871	hypothetical prote
7	1.6	100	2	S61050	probable membrane
8	1.6	112	2	C97787	hypothetical prote
9	1.6	116	2	F86676	hypothetical prote
10	1.6	122	2	E75377	hypothetical prote
11	1.6	158	2	E86498	hypothetical prote
12	1.6	158	2	E72124	pts IIA protein (1
13	1.6	164	2	E97061	Integrase XerD fam
14	1.6	183	2	A12419	hypothetical prote
15	1.6	185	2	H90463	hypothetical prote
16	1.6	197	2	A54506	tubulin alpha-1 ch
17	1.6	219	2	T19438	hypothetical prote
18	1.6	233	2	AD3344	hypothetical prote
19	1.6	237	2	C84976	tRNA (guanine-N1-)
20	1.6	240	2	A61544	tubulin alpha chal
21	1.6	264	2	A44959	coat protein - pot
22	1.6	267	2	A60366	coat protein - pot
23	1.6	267	2	S14001	genome polyprotein
24	1.6	267	2	S26630	capsid protein - p
25	1.6	267	2	JC1527	coat protein - pot
26	1.6	267	2	S13339	tail fiber protein
27	1.6	270	2	S73734	abc transport ATP-
28	1.6	273	2	C72328	transaminase B hom
29	1.6	287	2	A72421	oligopeptide ABC t

30	7	1.6	288	2	T36237	probable phosphot
31	7	1.6	306	2	T27985	hypothetical prote
32	7	1.6	307	2	B87659	hydrolase, probabl
33	7	1.6	310	2	T02200	probable RAV-like
34	7	1.6	313	2	JT0960	polyprotein - pota
35	7	1.6	321	2	H82240	conserved hypotet
36	7	1.6	324	2	T23876	hypothetical prote
37	7	1.6	326	2	A43939	proteinase inhibit
38	7	1.6	338	2	F69437	hypothetical prote
39	7	1.6	341	2	T47653	pectate lyase-like
40	7	1.6	342	2	G64411	hypothetical prote
41	7	1.6	342	2	C64394	hypothetical prote
42	7	1.6	343	2	AG2465	hypothetical prote
43	7	1.6	347	1	DNHUN2	NADH2 dehydrogenas
44	7	1.6	347	2	T11051	NADH2 dehydrogenas
45	7	1.6	347	2	B59153	NADH2 dehydrogenas

ALIGNMENTS

RESULT 1
E81195
phospholipase A1, probable NMB0464 [imported] - Neisseria meningitidis (strain MC58)
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: E81195
R:Retelien, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Oiu, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignanl, V.; Pizzi, M. Science 287, 1809-1815, 2000
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappaport, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; M0ID:2015755; PMID:10710307
A:Accession: E81195
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1382 <RET>
A:Cross-references: GB:AE002403; GB:AE002098; NID:g7225688; PIDN:AAF40901.1; PID:g722
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0464

Query Match 2.0%; Score 9; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 279 PEIFLTQPV 287
|||||||
DB 221 PEIFLTQPV 229

RESULT 2
H81831
probable phospholipase NMA2021 [imported] - Neisseria meningitidis (strain Z2491 serog
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
Holtroyd, S.; Jørgensen, K.; Leather, S.; Moutle, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: AB1775; M0ID:2022356; PMID:10761919
A:Accession: H81831
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <PAR>
A:Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85240.1; PID:g738
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA2021

Query Match 2.0%; Score 9; DB 2; Length 409;

Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 279 PEFITQPV 287
|||||
DB 248 PEFITQPV 256

RESULT 3

outer membrane phospholipase A (EC 3.1.1.-) precursor - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C>Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 18-Jun-1999
C:Accession: B36971; S40129
R:Brook, R.G.P.M.; Brinkman, E.; van Bortel, R.; Bekkers, A.C.A.P.A.; Verheij, H.M.; Tomm
J. Bacteriol. 176, 861-870, 1994
A:Title: Molecular characterization of enterobacterial plda genes encoding outer membran
A:Reference number: A36971; MUID:94131966; PMID:8300539
A:Accession: B36971
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <BRO>
A:Cross-references: EMBL:X76901; NID:9436880; PIDN:CAA54223.1; PID:9436881
A:Note: authors translated the codon AAG for residue 112 as Arg
C:Genetics:
A:Gene: plda
C:Superfamily: bacterial phospholipase A1
C:Keywords: carboxylic ester hydrolase

Query Match 1.8%; Score 8; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 GVGMLIND 438
|||||
DB 277 GVGMLIND 284

RESULT 4

RAV-like protein - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cross)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
R:Christians, N.; Robert, C.; Brotlier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, February 2000
A:Reference number: 224481
A:Accession: T47989
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <CHO>
A:Cross-references: EMBL:AL138642
A:Experimental source: cultivar Columbia; BAC clone F21F14
C:Genetics:
A:Map position: 3
A:Note: F21F14.140

Query Match 1.8%; Score 8; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 SLSFDLDR 181
|||||
DB 292 SLSFDLDR 299

RESULT 5

I-shaped tail fiber protein - phage T5
C:Species: phage T5
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000

C:Accession: S65934; S01984; S36851
R:Kallman, A.V.; Kulshin, V.E.; Shlyapnikov, M.G.; Ksenzenko, V.N.; Kryukov, V.M.
FEBS Lett. 366, 46-48, 1995
A:Title: The nucleotide sequence of the bacteriophage T5 ltf gene.
A:Reference number: S65934; MUID:95309401; PMID:7789514
A:Accession: S65934

A:Molecule type: DNA
A:Residues: 1-1396 <KAL>
A:Cross-references: EMBL:X69460; NID:g15415; PIDN:CAA49220.1; PID:g15416
R:Kallman, A.V.; Kryukov, V.M.; Bayev, A.A.
Nucleic Acids Res. 16, 6230, 1988
A:Title: The nucleotide sequence of bacteriophage T5 DNA at the region between early
A:Reference number: S01984; MUID:88289370; PMID:3267228
A:Accession: S01984
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 934-985, 'A', 987-1396 <KA2>
A:Cross-references: EMBL:X07559
C:Genetics:
A:Gene: ltf
C:Keywords: late protein; tail fiber

Query Match 1.8%; Score 8; DB 2; Length 1396;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QSATQSAS 61
|||||
DB 87 QSATQSAS 94

RESULT 6

hypothetical protein RC1370 [imported] - *Rickettsia conorii* (strain Malish 7)
C:Species: *Rickettsia conorii*
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: B97871
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <KUR>
A:Cross-references: GB:AE006914; PIDN:AAL03908.1; PID:g15620515; GSPDB:GN00173
C:Genetics:
A:Gene: RC1370

Query Match 1.6%; Score 7; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 TALENKT 84
|||||
DB 45 TALENKT 51

RESULT 7

probable membrane protein YDL163w - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein D1505
C:Species: *Saccharomyces cerevisiae*
C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 19-Apr-2002
C:Accession: S61050; S67715
R:POHL, T.M.
submitted to the EMBL Data Library, November 1995
A:Reference number: S61050
A:Accession: S61050
A:Molecule type: DNA
A:Residues: 1-100 <POH>
A:Cross-references: EMBL:Z67750; NID:g1061256; PID:g1061276
R:POHL, T.M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67708
A:Accession: S67715
A:Molecule type: DNA
A:Residues: 1-100 <POM>
A:Cross-references: EMBL:Z74212; NID:q1431258; PID:q1431260; MIPS:YDL163w
A:Experimental source: strain S286C
C:Genetics:
A:Cross-references: SGD:S0002322
A:Map position: 4L
C:Superfamily: Saccharomyces probable membrane protein YDL163w
C:Keywords: transmembrane protein
F:3-19/Domain: transmembrane #status predicted <TMM>

Query Match 1.6%; Score 7; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LTLSTLS 14
|||||
Db 26 LTLSTLS 32

RESULT 8

hypothetical protein RC0699 [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C:Accession: C97787
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fourmiller, P.E.; Barbe, V.; Samson, D.; Ro-
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: C97787
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-112 <KUR>
A:Cross-references: GB:AE006914; PIDN:AAI03237.1; PID:q15619790; GSPDB:GN00173
C:Genetics:
A:Gene: RC0699

Query Match 1.6%; Score 7; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 NDLGODN 47
|||||
Db 85 NDLGODN 91

RESULT 9

hypothetical protein ptca [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002
C:Accession: F86676
R:Boletín, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: F86676
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-116 <STO>
A:Cross-references: GB:AE005176; PID:q12723289; PIDN:AAK04512.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: ptca
C:Superfamily: phosphotransferase system lactose-specific enzyme II, factor III

Query Match 1.6%; Score 7; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 AIOQAKA 26
|||||
Db 34 AIOQAKA 40

RESULT 10

hypothetical protein - Deinococcus radiodurans (strain RJ)

C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: E75377
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Yamatchevan, J.-J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RJ.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75377
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-122 <WHI>
A:Cross-references: GB:AE002002; GB:AE000513; NID:q6459345; PIDN:AAF11150.1; PID:q645
C:Genetics:
A:Gene: DR1580
A:Map position: 1

Query Match 1.6%; Score 7; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 70 EHEPELY 76
|||||
Db 115 EHEPELY 121

RESULT 11

pts IIA Protein [imported] - Chlamydia pneumoniae (strain J138)

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: E86498
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: E86498
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <STO>
A:Cross-references: GB:BA000008; NID:q8978434; PIDN:BAA96271.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: ptsN.1
C:Superfamily: phosphotransferase system enzyme II, phosphotransferase system mannito

Query Match 1.6%; Score 7; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LSTLTLS 11
|||||
Db 126 LSTLTLS 132

RESULT 12

pts IIA protein - Chlamydia pneumoniae (strain CW4029)

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C:Accession: E72124
R:Kalmun, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,

Nature Genet. 21, 385-389, 1999
A>Title: Comparative genomes of *Claamydia pneumoniae* and *C. trachomatis*.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: E72124
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <ARN>
A:Cross-References: GB:AE001591; GB:AE001363; NID:g4376311; PIDN:AAD18213.1; PID:g437631
A:Experimental source: strain CML029
C:Genetics:
A:Gene: ptnN.1
C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannitol-5
F:28-156/Domain: phosphotransferase system mannitol-specific enzyme II factor III homolog

Query Match 1.6%; Score 7; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSTLTL 11
|||||
DB 126 LSTLTL 132

RESULT 13
E97061
Integrase XerD family protein (similarity only with C-terminal part) [Imported] - Clostr
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: E97061
R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97061
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-164 <KUR>
A:Cross-References: GB:AE001437; PIDN:AAK79280.1; PID:g15024240; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1310

Query Match 1.6%; Score 7; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 OLENKSN 378
|||||
DB 49 OLENKSN 55

RESULT 14
AI2419
hypothetical protein alr4913 [Imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A>Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AI2419
R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A>Title: Complete Genome Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AI2419
A:Molecule type: DNA
A>Status: preliminary
A:Residues: 1-183 <KUR>
A:Cross-References: GB:BA000019; PIDN:BAW6612.1; PID:g17134051; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr4913

Query Match 1.6%; Score 7; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 EVRSEND 42
|||||
DB 104 EVRSEND 110

RESULT 15
H90463
hypothetical protein SSO2858 [Imported] - *Sulfolobus solfataricus*
C:Species: *Sulfolobus solfataricus*
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: H90463
R.She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to Genbank, April 2001
A:Description: *Sulfolobus solfataricus* complete genome.
A:Reference number: A99139
A:Accession: H90463
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-185 <KUR>
A:Cross-References: GB:AE006641; NID:g13816218; PIDN:AAK42967.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO2858

Query Match 1.6%; Score 7; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LTLTL 14
|||||
DB 122 LTLTL 128

Search completed: November 12, 2002, 11:46:31
Job time : 14.75 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:45 ; Search time 7.5 Seconds

(without alignments)
2444.338 Million cell updates/sec

Title: us-09-787-083-6

Perfect score: 442
Sequence: 1 MKVSLSTLRLSLSCFAALLA.....YNHKATSPGVGLMLNDMMGL 442

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	1.8	286	1	PAL_KLEPN
2	8	1.8	1396	1	VLTF_BPPT5
3	7	1.6	197	1	TBA_PLAYO
4	7	1.6	212	1	PRL_ICTPU
5	7	1.6	237	1	TRMD_BUCAL
6	7	1.6	240	1	TBA_OCTVU
7	7	1.6	270	1	Y304_MYCPN
8	7	1.6	273	1	LIVE_THEMA
9	7	1.6	322	1	MTAA_PSEPU
10	7	1.6	326	1	SPI_BACBR
11	7	1.6	342	1	FLAD_METJA
12	7	1.6	342	1	Y755_METJA
13	7	1.6	347	1	NU2M_CAPII
14	7	1.6	347	1	NU2M_HUMAN
15	7	1.6	347	1	NU2M_PANTR
16	7	1.6	347	1	NU2M_PONPA
17	7	1.6	347	1	NU2M_SHEEP
18	7	1.6	423	1	AMT_AOUAE
19	7	1.6	444	1	TBA_ONCKE
20	7	1.6	448	1	TBA4_HUMAN
21	7	1.6	448	1	TBA5_HUMAN
22	7	1.6	449	1	TBA2_DROME
23	7	1.6	449	1	TBAE_PHYPO
24	7	1.6	449	1	TBAN_PHYPO
25	7	1.6	449	1	TBA_XENLA
26	7	1.6	450	1	TBAD_PHYPO
27	7	1.6	450	1	TBA_HABCO
28	7	1.6	450	1	TBA_NOTVI
29	7	1.6	451	1	TBA1_HUMAN
30	7	1.6	451	1	TBA3_HUMAN
31	7	1.6	451	1	TBA_OCTDO
32	7	1.6	451	1	TBA_TORMA
33	7	1.6	511	1	LGT_CITUN

34	7	1.6	513	1	ATPA_HAEIN	P43714	haemophilus
35	7	1.6	536	1	60IM_BUCAP	P29431	buchnera ap
36	7	1.6	544	1	GP10_DICDI	O06885	dictyostell
37	7	1.6	567	1	GPV_RAT	O08770	rattus norv
38	7	1.6	610	1	FIMB_DICDI	P54680	dictyostell
39	7	1.6	681	1	CAO2_HUMAN	O99424	homo sapien
40	7	1.6	768	1	YB23_HUMAN	O9U117	homo sapien
41	7	1.6	783	1	FTB_HUMAN	O15117	homo sapien
42	7	1.6	824	1	TG37_MOUSE	O61371	mus musculu
43	7	1.6	862	1	AXN1_HUMAN	O15169	homo sapien
44	7	1.6	947	1	LKTA_PASBP	P55123	pasteurella
45	7	1.6	1026	1	VG37_BPPT4	P03744	bacterioph

ALIGNMENTS

```

RESULT 1
PAL_KLEPN
ID PAL_KLEPN STANDARD; PRT; 286 AA.
AC P37446;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Phospholipase A1 precursor (EC 3.1.1.32) (Detergent-resistant
DE phospholipase A) (DR-phospholipase A) (Phosphatidylcholine 1-
DE acylhydrolase) (Outer membrane phospholipase A) (OM PLA).
GN PLDA.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94131966; PubMed=8300539;
RA Brock R.G.P.M., Brinkman E., van Borel R., Bekkers A.C.A.P.,
RA Verheij H.M., Tommassen J.;
RT "Molecular characterization of enterobacterial plda genes encoding
RT outer membrane phospholipase A."
RL J. Bacteriol. 176:861-870(1994).
CC -1- FUNCTION: HYDROLYSIS OF PHOSPHATIDYLCHOLINE WITH PHOSPHOLIPASE
CC A2 (EC 3.1.1.4) AND PHOSPHOLIPASE A1 (EC 3.1.1.32) ACTIVITIES.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 2-
CC acylglycerophosphocholine + a fatty acid anion.
CC -1- COFACTOR: REQUIRES CALCIUM IONS FOR ACTIVITY.
CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE; ONE OF THE VERY FEW ENZYMES
CC LOCATED THERE.
CC -----
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CC -----
CC EMBL: X76901; CA54223.1; -
CC PIR: B36971; B36971.
CC PIR: S40129; S40129.
CC HSSP: P00631; I0D6.
CC InterPro: IPR003187; PLA1.
CC Pfam: PF02253; PLA1; 1.
CC PRINTS: PR01486; PHPLIPASEA1.
KW Hydrolyase; Lipid degradation; Outer membrane; Signal; Calcium.
FT SIGNAL 1 20
FT CHAIN 21 286
FT ACT_SITE 161 161
FT SEQUENCE 286 AA; 32544 MW; 3E39F863085108A3 CRC64;
Query Match 1.8%; Score 8; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6;

```

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 431 GVGMLND 438
 |||||
 RN 277 GVGMLND 284

RESULT 2
 ID VUT5_BPT5 STANDARD; PRT: 1396 AA.
 AC P13390; 048502;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE L-shaped tail fiber protein (LTF protein).
 GN LTF.
 OS Bacteriophage T5.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC T5-like viruses.
 OX NCBI_Taxid=10726;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95309401; Pubmed=7789514;
 RA Kallman A.V., Kulshin V.E., Shlyapnikov M.G., Keenzenko V.N.,
 RA Kryukov V.M.;
 RT "The nucleotide sequence of the bacteriophage T5 ltf gene."
 RL FEBS Lett. 366:46-48(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Kallman A.V.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE=88289370; Pubmed=3267228;
 RA Kallman A.V., Kryukov V.M., Bayev A.A.;
 RT "The nucleotide sequence of bacteriophage T5 DNA at the region
 RT between early and late genes".
 RL Nucleic Acids Res. 16:6230-6230(1988).
 CC -1- FUNCTION: NONESSENTIAL PROTEIN THAT MEDIATES BINDING TO THE
 CC POLYMANNOSE O ANTIGEN.
 CC -----
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 CC -----
 DR EMBL: X69460; CAA49220.1; -.
 DR EMBL: A0001191; CAA04591.1; -.
 DR PIR: S01982; S01982.
 KW Late protein.
 FT CONFILICT 986 V -> A (IN REF. 2).
 SQ SEQUENCE 1396 AA; 147989 MW; 18CD2192F65FFC1 CRC64;

Query Match 1.6%; Score 8; DB 1; Length 1396;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 QSATOSAS 61
 |||||
 DB 87 QSATOSAS 94

RESULT 3
 ID TBA_PLAYO STANDARD; PRT: 197 AA.
 AC P12543;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Tubulin alpha chain (Fragment).

OS Plasmodium berghei yoelli.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_Taxid=5862;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89014607; Pubmed=2459618;
 RA Akella R., Arasu P., Vaideya A.B.;
 RT "Molecular clones of alpha-tubulin genes of Plasmodium yoelli reveal
 RT an unusual feature of the carboxy terminus."
 RL Mol. Biochem. Parasitol. 30:165-174(1988).
 CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
 CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
 CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
 CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: M29816; AAA29779.1; -.
 DR PIR: A54506; A54506.
 DR InterPro: IPR000217; Tubulin.
 DR InterPro: IPR003008; Tubulin_FtsZ.
 DR Pfam: PF00091; tubulin; 1.
 DR PROSITE: PS00227; TUBULIN; PARTIAL.
 KW Microtubules; GTP-binding.
 FT NON_TER 1
 SQ SEQUENCE 197 AA; 22111 MW; 4DAAF199CC6CD319 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 IKTKRSI 120
 |||||
 DB 82 IKTKRSI 88

RESULT 4
 ID PRL_ICTPU STANDARD; PRT: 212 AA.
 AC P51904; 091819;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Prolactin precursor (PRL).
 GN PRL.
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OX NCBI_Taxid=7998;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Plutitary;
 RA Tang Y.;
 RT "A study on the channel catfish (Ictalurus punctatus) growth hormone
 RT gene family: structures of growth hormone and prolactin genes and
 RT somatolactin cDNA, their evolutionary implications and expression in
 RT the pituitary gland."
 RL Thesis (1993), University of Maryland, U.S.A.
 RN (2)
 RP SEQUENCE OF 27-212 FROM N.A.
 RC TISSUE=Plutitary;
 RX MEDLINE=93364578; Pubmed=1308206;
 RA Watanabe K., Igarashi A., Noso T., Chen T.T., Dunham R.A.,
 RA Kawachi H.;
 RT "Chemical identification of catfish growth hormone and prolactin.";

```

RL Mol. Mar. Biol. Biotechnol. 1:239-249(1992).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PITUITARY GLANDS.
CC -1- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
-----
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-----
DR EMBL: AF267990: AAF82287.1; -.
DR HSSP: Q28632: IAN3.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF00103; hormone; 2.
DR PRINTS: PR00836; SOMATOTROPIN.
DR PROSITE: PS00266; SOMATOTROPIN_1; 1.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
KW Hormone; pituitary; signal.
FT SIGNAL 1 26
FT CHAIN 27 212 PROLACTIN.
FT DISULEID 71 185 BY SIMILARITY.
FT DISULEID 202 212 G -> S (IN REF. 2).
FT CONFLICT 91 91 T -> S (IN REF. 2).
FT CONFLICT 128 128 D -> R (IN REF. 2).
FT CONFLICT 203 203
SQ SEQUENCE 212 AA; 23365 MW; 073FB7FBD573BE CRC64;

Query Match
Best Local Similarity 1.6%; Score 7; DB 1; Length 212;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 NDGQDN 47
Db 166 NDGQDN 172

RESULT 5
TID TBA_BUCAI STANDARD; PRT; 237 AA.
AC P57476;
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE tRNA (Guanine-N(1)-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
DE TRMD OR BU396.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT Buchnera sp. APS.;
RL Nature 407:81-86(2000).
CC -1- FUNCTION: SPECIFICALLY METHYLATES GUANOSINE-37 IN VARIOUS TRNAS
CC (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA - S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
-----
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-----
DR EMBL: AP001119; BAB13099.1; -.
DR InterPro: IPR002649; tRNA_mIG_MT.
DR Pfam: PF01746; tRNA_mIG_MT; 1.
DR PRODOM: PD004978; tRNA_mIG_MT; 1.
DR TIGRFAMs: TIGR00088; trnd; 1.
KW Transferase; Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 237 AA; 27335 MW; 86CE3836B35EC4AB CRC64;

Query Match
Best Local Similarity 1.6%; Score 7; DB 1; Length 237;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LAIQAK 25
Db 78 LAIQAK 84

RESULT 6
TID TBA_OCTVU STANDARD; PRT; 240 AA.
AC P24635;
DT 01-MAR-1992 (Rel. 21; Created)
DT 01-MAR-1992 (Rel. 21; Last sequence update)
DT 15-JUL-1999 (Rel. 38; Last annotation update)
DE Tubulin alpha chain (Fragment).
DE Octopus vulgaris (Octopus).
OS Eukaryota; Metazoa; Mollusca; Cephalopoda; coleidea; Octopoda;
OC Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=6645;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RA Zinov'Eva R.D., Aleinikova K.S., Tomarev S.I.;
RT "Isolation and structural characterization of cDNAs coding for alpha-
RT tubulin of the octopus eye lens.";
RL Dokl. Akad. Nauk SSSR 302:462-467(1988).
CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
-----
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-----
DR EMBL: X15845; CAA33844.1; -.
DR PIR: A61544; A61544.
DR InterPro: IPR000217; Tubulin.
DR InterPro: IPR003008; Tubulin_FtsZ.
DR Pfam: PF00091; tubulin; 1.
DR PROSITE: PS00227; TUBULIN; PARTIAL.
KW Microtubules; GTP-binding.
FT NON_TER 1 1
FT SITE 240 240 INVOLVED IN POLYMERIZATION.
SQ SEQUENCE 240 AA; 26961 MW; 13BB3A1F740F2416 CRC64;

Query Match
Best Local Similarity 1.6%; Score 7; DB 1; Length 240;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 IKTKRSI 120
Db 124 IKTKRSI 130

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RESULT 7
ID Y304_MYCPN STANDARD: PRT: 270 AA.
AC P75355;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical ABC transporter ATP-binding protein MG304 homolog
DE (A05-grf270L).
GN MPN433 OR MP408.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
CX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirk E., Li B.-C.,
  Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
  pneumoniae."
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
-----
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-----
CC
CC EMBL: AE000040; AAB96056.1; -.
DR InterPro: IPR003593; AAA_Artpase.
DR InterPro: IPR003439; ABC_transporter.
DR Pfam: PF00005; ABC_tran. 1.
DR ProDom: PD000006; ABC_transportr; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
DR Hypothetical protein; ATP-binding; Transport; Complete proteome.
KW NP_BIND 36 43 ATP (POTENTIAL).
FT SEQUENCE 270 AA: 30770 MW: 6512640E4BC051B4 CRC64;
SQ
Query Match 1.6%; Score 7; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 168 KQFPLS 174
DB 125 KQFPLS 131

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RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
  Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
  Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
  genome sequence of Thermotoga maritima."
RL Nature 399:323-329(1999).
RN [2]
RP SEQUENCE OF 68-273 FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=97017137; PubMed=8863738;
RA Guipaud O., Labedan B., Forterre P.;
RT "A gyrB-like gene from the hyperthermophilic bacterium Thermotoga
  maritima."
RL Gene 174:121-128(1996).
CC -1- FUNCTION: Acts on leucine, isoleucine and valine (by similarity).
CC -1- CATALYTIC ACTIVITY: L-leucine + 2-oxoglutarate = 4-methyl-2-
  oxopentanoate + L-glutamate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: Valine and isoleucine biosynthesis.
CC -1- SIMILARITY: BELONGS TO CLASS-IV OF PYRIDOXAL-PHOSPHATE-DEPENDENT
  AMINOTRANSFERASES.
-----
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-----
CC
CC EMBL: AE001750; AAD35913.1; -.
DR EMBL: U49692; AAC44497.1; -.
DR HSSP: P00510; IA3G.
DR TIGR: TM0831; -.
DR InterPro: IPR001544; Aminotran_4.
DR Pfam: PF01063; aminotran_4; 1.
DR ProDom: PD001961; Aminotran_4; 1.
DR PROSITE: PS00770; AA_TRANSFER_CLASS_4; 1.
DR Transferase; Aminotransferase; Branched-chain amino acid biosynthesis;
  Pyridoxal phosphate; Complete proteome.
KW CONFLICT 77 77 A -> R (IN REF. 2).
FT SEQUENCE 273 AA: 31158 MW: 21628705612E90E3 CRC64;
SQ
Query Match 1.6%; Score 7; DB 1; Length 273;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 PLTSLFD 178
DB 61 PLTSLFD 67

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RESULT 8
ID ILVE_THEME STANDARD: PRT: 273 AA.
AC P74921;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable branched-chain amino acid aminotransferase (EC 2.6.1.42)
DE (BCAT).
GN ILVE OR TM0831.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
  Thermotogaceae; Thermotoga.
CX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
  Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
  McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

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RA MIAA_PSEPU STANDARD: PRT: 322 AA.
AC O30762;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (IPP
  transferase) (isopentenyl-diphosphate:tRNA isopentenyltransferase)
DE (IPPTase) (IPPT).
GN MIAA.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
  Pseudomonas.
CX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M;
RA Olekhnovich I.N., Gussin G.N.;
RT "Attenuation of the Pseudomonas putida trpE and trpGDC genes."
  Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

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CC -1- FUNCTION: CATALYZES THE FIRST STEP IN THE BIOSYNTHESIS OF
CC 2-METHYLTHIO-N6-(DELR(2)-ISOPENTENYL)-ADENOSINE (MS211[6A])
CC ADVANCE TO THE ANTICODON OF SEVERAL tRNA SPECIES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: isopentenyl diphosphate + tRNA - diphosphate +
CC tRNA containing 6-isopentenyladenosine.
CC -1- SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
CC -----
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CC -----
DR EMBL; AF016312; AAB69443.1; -
DR InterPro; IPR002627; IPT.
DR Pfam; PF01715; IPT.1.
DR ProDom; PD004674; IPT.1.
DR TIGRfam; TIGR00174; miaa.1.
DR Transferase; Nucleotidylyltransferase; tRNA processing; ATP-binding.
KW NP_BIND 12 19 ATP (POTENTIAL).
SQ SEQUENCE 322 AA; 35488 MW; D1AA81A2D7B32FE6 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 322;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 FVDEVRS 39
|111111
Db 231 FVDEVRS 237

RESULT 10
SPI_BACBR ID SPI_BACBR STANDARD; PRT; 326 AA.
AC P43131;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Protease inhibitor precursor (BBRP1).
OS Bacillus brevis.
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
OX NCBI_TaxID=1393;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-32; 104-112 AND 122-136.
RC STRAIN=HPD31;
RA MEDLINE=92304060; Pubmed=1610177;
RA Shiga Y., Hasegawa K., Tsuboi A., Yamagata H., Ueda S.;
RT "Characterization of an extracellular protease inhibitor of Bacillus
RT brevis HPD31 and nucleotide sequence of the corresponding gene.";
RL Appl. Environ. Microbiol. 58:525-531(1992).
CC -1- FUNCTION: SHOWS INHIBITORY ACTIVITY TOWARDS SERINE PROTEASES, SUCH
CC AS TRYPSIN, CHYMOTRYPSIN, AND SUBTILISIN. MAY FORM A TRYPSIN-
CC INHIBITOR COMPLEX IN A MOLAR RATIO OF 1:1. IT IS HEAT RESISTANT AT
CC NEUTRAL AND ACIDIC pHs.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: MAY UNDERGO ACTIVATION AFTER SECRETION. IT IS PRODUCED
CC EXTRACELLULARLY IN MULTIPLE FORMS HAVING AT LEAST THREE DIFFERENT
CC MOLECULAR WEIGHTS (BBRP1-A, -B, AND -C).
CC -----
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CC -----
DR EMBL; D10696; BAA01538.1; -
KW Serine protease inhibitor; Protease inhibitor; signal; Repeat.
FT SIGNAL 1 24
FT CHAIN 25 326 SERINE PROTEASE INHIBITOR.

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FT CHAIN 104 326 SERINE PROTEASE INHIBITOR-C. (POTENTIAL).
FT CHAIN 104 ? SERINE PROTEASE INHIBITOR-B. (POTENTIAL).
FT CHAIN 122 326 SERINE PROTEASE INHIBITOR-A.
FT DOMAIN 177 304 CONTAINS TWO APPROXIMATE REPEATS.
FT REPEAT 177 208 1.
FT REPEAT 272 304 2.
SQ SEQUENCE 326 AA; 35100 MW; 1C0456ABFA912F77 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 326;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 PVAFVDE 36
|111111
Db 119 PVAFVDE 125

RESULT 11
FLAD_METUA ID FLAD_METUA STANDARD; PRT; 342 AA.
AC Q58305;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative flagella-related protein D.
GN FLAD OR M0895.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; Pubmed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,
RA Uitterlinden T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: STRONG. TO M. VOLTAE FLAD, ALSO TO FLAE.
CC -----
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CC -----
DR EMBL; U67533; AAB98898.1; -
DR TIGR; M0895; -
KW Flagella; Complete proteome.
SQ SEQUENCE 342 AA; 39950 MW; B384DDDE1775566C CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 342;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PDILDDY 362
|111111
Db 255 PDILDDY 261

RESULT 12
Y755_METUA ID Y755_METUA STANDARD; PRT; 342 AA.
AC Q58165;

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DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0755 precursor.
GN MJ0755.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
ON NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reisch C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Melman J.F., Fuhrman J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RT Science 273:1058-1073(1996).
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CC -----
DR EMBL: U67521; AAB98748.1; -
DR TIGR: MJ0755; -
KM Hypothetical protein: Signal: Complete proteome.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 342 HYPOTHETICAL PROTEIN MJ0755.
SQ SEQUENCE 342 AA; 38778 MW; BD25220A7EBAD85C CRC64;

Query Match 1.6%; Score 7; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 76 YTTALEN 82
    |||||
Db 90 YTTALEN 96

RESULT 13
NU2M_CAPHI
ID NU2M_CAPHI STANDARD; PRT; 347 AA.
AC Q36346;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
GN MTND2 OR ND2.
OS Capra hircus (Goat).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
ON NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Dove P., Mann W., Hecht W.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone -> NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X72965; CA51468.1; -
DR InterPro: IPR003917; NADhub.Oxred2.
DR InterPro: IPR001750; Oxidored_q1.
DR Pfam: PF00361; Oxidored_q1.1.
DR PRINTS: PR01436; NADHDCGNASE2.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SQ SEQUENCE 347 AA; 39136 MW; 6129CF9080475E CRC64;

Query Match 1.6%; Score 7; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 LTLSTLS 14
    |||||
Db 155 LTLSTLS 161

RESULT 14
NU2M_HUMAN
ID NU2M_HUMAN STANDARD; PRT; 347 AA.
AC P03881; Q34769; Q9TGT0; Q9TGT1; Q9TGT2; Q9TGT3; Q9TGT4;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
GN MTND2 OR ND2.
OS Homo sapiens (human).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=81173052; PubMed=7219534;
RA Anderson S., Bankier A.T., Barrell B.G., de Bruijn M.H.L.,
RA Coulson A.R., Drouin J., Eperon I.C., Nierlich D.P., Roe B.A.,
RA Sanger F., Schreier P.H., Smith A.J.H., Staden R., Young I.G.;
RT "Sequence and organization of the human mitochondrial genome.";
RL Nature 290:457-465(1981).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=81170577; PubMed=6260957;
RA Sanger F., Coulson A.R., Barrell B.G., Smith A.J.H., Roe B.A.;
RT "Cloning in single-stranded bacteriophage as an aid to rapid DNA
RT sequencing.";
RL J. Mol. Biol. 143:161-178(1980).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS V-69; S-88; D-150; M-237; T-265;
RP T-278; V-265 AND A-333.
RA MEDLINE=98133898; PubMed=9475751;
RA Wise C.A., Sraml M., Eastaugh S.;
RT "Departure from neutrality at the mitochondrial NADH dehydrogenase
RT subunit 2 gene in humans, but not in chimpanzees.";
RL Genetics 148:409-421(1998).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS ILE-43; LEU-325 AND THR-331.
RC TISSUE=Placenta;
RA MEDLINE=95132634; PubMed=7530363;
RA Horai S., Hayasaka K., Kondo R., Tsugane K., Takahata N.;
RT "Recent African origin of modern humans revealed by complete sequences
RT of hominoid mitochondrial DNAs.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:532-536(1995).
RN [5]
RP IDENTIFICATION OF PROTEIN.

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RX MEDLINE=85188293; PubMed=3921850;
 RA Choum A., Mariotti P., Cleeter M.W.J., Ragan C.I., Matsuno-Yagi A.,
 RA Hateli Y., Doolittle R.F., Altardi G.;
 RT "Six unidentified reading frames of human mitochondrial DNA encode
 RT components of the respiratory-chain NADH dehydrogenase.";
 RL Nature 314:592-597(1985).
 RN [6]
 RP VARIANT LHON ASP-150.
 RX MEDLINE=91144615; PubMed=1900003;
 RA Johns D.R., Berman J.;
 RT "Alternative, simultaneous complex I mitochondrial DNA mutations in
 RT Leber's hereditary optic neuropathy.";
 RL Biochem. Biophys. Res. Commun. 174:1324-1330(1991).
 RN [7]
 RP VARIANTS L-42; R-63; A-119; P-148; S-150; T-159 AND A-185.
 RX MEDLINE=92098084; PubMed=1757091;
 RA Marzuki S., Noer A.S., Lertit P., Thyagarajan D., Kapra R.,
 RA Utthanaphol P., Byrne E.;
 RT "Normal variants of human mitochondrial DNA and translation products:
 RT the building of a reference data base.";
 RL Hum. Genet. 88:139-145(1991).
 RN [8]
 RP VARIANT LHON SER-259.
 RX MEDLINE=92120513; PubMed=1732158;
 RA Brown M.D., Voljavec A.S., Lott M.T., Torroni A., Yang C.C.,
 RA Wallace D.C.;
 RT "Mitochondrial DNA complex I and III mutations associated with
 RT Leber's hereditary optic neuropathy.";
 RL Genetics 130:163-173(1992).
 RN [9]
 RP VARIANT AD SER-331.
 RX MEDLINE=92118019; PubMed=1370613;
 RA Lin F.-H., Lin R., Wisniewski H.M., Hwang Y.-W., Grundke-Iqbal I.,
 RA Healy-Louie G., Iqbal K.;
 RT "Detection of point mutations in codon 331 of mitochondrial NADH
 RT dehydrogenase subunit 2 in Alzheimer's brains.";
 RL Biochem. Biophys. Res. Commun. 182:238-246(1992).
 RN [10]
 RP VARIANT THR-57.
 RX MEDLINE=98127994; PubMed=9461455;
 RA Rieder M.J., Taylor S.L., Toke V.O., Nickerson D.A.;
 RT "Automating the identification of DNA variations using quality-based
 RT fluorescence re-sequencing: analysis of the human mitochondrial
 RT genome.";
 RL Nucleic Acids Res. 26:967-973(1998).
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DISEASE: DEFECTS IN MTND2 ARE ONE OF THE CAUSES OF LEBER'S
 CC HEREDITARY OPTIC NEUROPATHY (LHON), A MATERNALLY INHERITED DISEASE
 CC RESULTING IN ACUTE BILATERAL BLINDNESS DUE TO RETINAL DEGENERATION
 CC PREDOMINANTLY IN YOUNG MEN. CARDIAC CONDUCTION DEFECTS AND
 CC NEUROLOGICAL DEFECTS HAVE ALSO BEEN DESCRIBED. RESULTING IN OPTIC
 CC NERVE DEGENERATION AND CARDIAC DYSRHYTHMIA.
 CC -1- DISEASE: DEFECTS IN MTND2 COULD BE ASSOCIATED WITH ALZHEIMER'S
 CC DISEASE (AD).
 CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
 CC -----
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 CC -----
 DR EMBL: J01415; AAB58944.1; -;
 DR EMBL: V00662; CAA24027.1; -;
 DR EMBL: M10546; AAB55502.1; ALT_INIT.
 DR EMBL: D38112; BAA07291.1; -;
 DR EMBL: AF014882; AAC25441.1; -;
 DR EMBL: AF014884; AAC25443.1; -;
 DR EMBL: AF014885; AAC25444.1; -;

DR EMBL: AF014887; AAC25446.1; -;
 DR EMBL: AF014889; AAC25448.1; -;
 DR EMBL: AF014890; AAC25449.1; -;
 DR EMBL: AF014891; AAC25450.1; -;
 DR EMBL: AF014892; AAC25451.1; -;
 DR EMBL: AF014895; AAC25454.1; -;
 DR EMBL: AF014896; AAC25455.2; -;
 DR EMBL: AF014897; AAC25456.1; -;
 DR EMBL: AF014898; AAC25457.1; -;
 DR EMBL: AF014899; AAC25458.2; -;
 DR EMBL: AF014900; AAC25459.1; -;
 DR EMBL: AF014901; AAC25460.1; -;
 DR PIR: A00414; DNHMN2.
 DR Genew; HGNC:7456; MTND2.
 DR MIM: 502500; -;
 DR MIM: 516001; -;
 DR MIM: 535000; -;
 DR InterPro: IPR003917; NADHoxred2.
 DR InterPro: IPR001750; Oxidored_q1.
 DR Pfam: PF00361; Oxidored_q1; 1.
 DR PRINTS; PRO1436; NADHGNASE2.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane;
 KW Disease mutation; Leber's hereditary optic neuropathy;
 KW Alzheimer's disease; Polymorphism.
 FT VARIANT 42 42
 P -> L.
 /FTId-VAR_008590.
 V -> I.
 /FTId-VAR_011348.
 I -> T.
 /FTId-VAR_008591.
 O -> R.
 /FTId-VAR_008592.
 I -> V.
 /FTId-VAR_011349.
 N -> S.
 /FTId-VAR_011350.
 T -> A.
 /FTId-VAR_008593.
 S -> P.
 /FTId-VAR_008594.
 N -> D (IN LHON; SECONDARY MUTATION; DOES
 NOT SEEM TO DIRECTLY CAUSE THE DISEASE).
 /FTId-VAR_004755.
 N -> S.
 /FTId-VAR_008595.
 I -> T.
 /FTId-VAR_008596.
 T -> A.
 /FTId-VAR_008597.
 L -> M.
 /FTId-VAR_011351.
 G -> S (IN AD); RARE PRIMARY MUTATION).
 /FTId-VAR_004756.
 A -> T.
 /FTId-VAR_011352.
 A -> V.
 /FTId-VAR_011353.
 I -> T.
 /FTId-VAR_011354.
 F -> L.
 /FTId-VAR_011355.
 A -> S (IN AD).
 /FTId-VAR_004758.
 A -> T.
 /FTId-VAR_004757.
 T -> A.
 /FTId-VAR_011356.
 FT SEQUENCE 347 AA; 38961 MW; C06FD962317C3F2D CRC64;
 SQ
 Query Match 1.6%; Score 7; DB 1; Length 347;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LFLSILS 14
| | | | |
Db 155 LFLSILS 161

RESULT 15

NU2M_PANTR
ID NU2M_PANTR STANDARD; PRT; 347 AA.

AC O21798;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).

GN MTND2 OR ND2.

OS Pan troglodytes (Chimpanzee).

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.

OX NCBI_TaxID=9598;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98133898; PubMed=9475751;

RA Wise C.A., Strahl M., Easton S.;

RT "Departure from neutrality at the mitochondrial NADH dehydrogenase
subunit 2 gene in humans, but not in chimpanzees.";

RL Genetics 148:409-421(1998).

CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.

CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.

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CC -----

DR EMBL; AF014908; AAC25467.1; -

DR EMBL; AF014909; AAC25468.1; -

DR EMBL; AF014910; AAC25469.1; -

DR EMBL; AF014911; AAC25470.1; -

DR EMBL; AF014912; AAC25471.1; -

DR EMBL; AF014913; AAC25472.1; -

DR EMBL; AF014914; AAC25473.1; -

DR EMBL; AF014915; AAC25474.1; -

DR EMBL; AF014916; AAC25475.1; -

DR EMBL; AF014917; AAC25476.1; -

DR EMBL; AF014918; AAC25477.1; -

DR EMBL; AF014919; AAC25478.1; -

DR EMBL; AF014920; AAC25479.1; -

DR EMBL; AF014921; AAC25480.1; -

DR InterPro: IPR003917; NADH_oxred2.

DR InterPro: IPR001750; Oxidored_g1.

DR Pfam: PF00361; Oxidored_g1.1.

DR PRINTS: PR01436; NADH6NASE2.

KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.

FT VARIANT 94 94 P -> S (IN STRAIN A-292).

SQ SEQUENCE 347 AA; 39020 MW; 2E8269D105810D4E CRC64;

Query Match 1.6%; Score 7; DB 1; Length 347;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LFLSILS 14
| | | | |
Db 155 LFLSILS 161

Search completed: November 12, 2002, 11:45:30
Job time : 9.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:46 : Search time 26.25 Seconds
(without alignments)
3469.441 Million cell updates/sec

Title: US-09-787-083-6
Perfect score: 442
Sequence: 1 MKVSLSTLSTLSLSCFAILA.....YNHEATSPFGVGLINDMNGL 442

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp rodent:*
12: sp.virus:*
13: sp vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	2.0	382	16	Q9K0U7
2	9	2.0	409	16	Q9K0U7
3	9	2.0	409	16	Q9K0U7
4	9	2.0	409	16	Q9K0U7
5	8	1.8	227	17	Q8RTU3
6	8	1.8	227	17	Q8RTU3
7	8	1.8	227	17	Q8RTU3
8	8	1.8	227	17	Q8RTU3
9	8	1.8	227	17	Q8RTU3
10	8	1.8	227	17	Q8RTU3
11	8	1.8	227	17	Q8RTU3
12	8	1.8	227	17	Q8RTU3
13	8	1.8	227	17	Q8RTU3
14	8	1.8	227	17	Q8RTU3
15	8	1.8	227	17	Q8RTU3
16	8	1.8	227	17	Q8RTU3

17	7	1.6	112	16	Q92HS2
18	7	1.6	116	16	Q9CIE9
19	7	1.6	122	16	Q9RU16
20	7	1.6	124	12	Q91ZS7
21	7	1.6	131	6	Q9GMD4
22	7	1.6	138	12	Q91ZQ7
23	7	1.6	142	16	Q8RAS3
24	7	1.6	147	5	Q36035
25	7	1.6	158	16	Q929C1
26	7	1.6	164	16	Q97JH4
27	7	1.6	169	16	Q9L2A7
28	7	1.6	183	16	Q8YMM0
29	7	1.6	185	17	Q97UY1
30	7	1.6	189	13	Q9DPT2
31	7	1.6	198	4	Q9BUX9
32	7	1.6	200	5	Q8T2L3
33	7	1.6	212	13	Q90ZNS
34	7	1.6	214	5	Q9VTR5
35	7	1.6	216	2	Q9X6H6
36	7	1.6	218	2	Q9RRT4
37	7	1.6	219	5	Q17594
38	7	1.6	220	2	Q9XCX1
39	7	1.6	221	5	Q36036
40	7	1.6	221	12	Q65002
41	7	1.6	227	5	Q9BME4
42	7	1.6	233	6	Q9WZB0
43	7	1.6	233	16	Q8YH08
44	7	1.6	236	13	Q9DPS8
45	7	1.6	264	12	Q85260

ALIGNMENTS

RESULT 1
Q9K0U7 PRELIMINARY; PRT; 382 AA.
AC Q9K0U7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Phospholipase A1, putative.
GN NMB0464
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-MC58 / SEROGROUP B:
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B., Cotton M.D., Uitterlind T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scariato V., Maignani V., Piza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappelli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58."
RL Science 287:1809-1815(2000).
DR EMBL: AE002403; AAF40901.1;
DR HSSP: P00631; IQD5.
DR TIGR: NMB0464;
DR InterPro: IPR003187; PLAI.
DR Pfam: PF02253; PLAI; 1.
KW Complete proteome.
SQ SEQUENCE 382 AA; 42714 MW; B468A802F052EB36 CRC64;
Query Match 2.0%; Score 9; DB 16; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 279 PEIFLTPV 287
 DB 221 PEIFLTPV 229

RESULT 2

ID 09J721 PRELIMINARY: PRT: 409 AA.

AC 09J721: 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Putative phospholipase.

GN MA2021.

OS Neisseria meningitidis (serogroup A).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=65699;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;

RA MEDLINE=20222556; PubMed=10761919;

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

RA Whitehead S., Spratt B.G., Barrall B.G.;

RT "Complete DNA sequence of a serogroup A strain of Neisseria

RT meningitidis Z2491."

RL Nature 404:502-506(2000).

DR EMBL: AL162757; CAB85240.1;

DR HSRP: P00631; IQD5.

DR InterPro: IPR003187; PLA1.

DR Pfam: PF02253; PLA1; 1.

KW Complete proteome.

SQ SEQUENCE 409 AA; 45862 MW; CD6585B064D01A41 CRC64;

Query Match 2.0%; Score 9; DB 16; Length 409;

Best Local Similarity 100.0%; Pred. No. 1.9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 279 PEIFLTPV 287

DB 248 PEIFLTPV 256

RESULT 3

O9CL62 PRELIMINARY: PRT: 862 AA.

AC 09CL62: 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE CVG8Y.

GN CVG8Y OR PM1380.

OS Pasteurella multocida.

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;

OC Pasteurella.

OX NCBI_TaxID=747;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PM70;

RA MEDLINE=2114566; PubMed=11248100;

RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

RA "Complete genomic sequence of Pasteurella multocida pm70."

RA Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

CC -1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER

CC REGULATORY COMPONENTS OF SENSOR TRANSDUCTION SYSTEMS.

CC EMBL: AE006176; AAK03464.1;

DR InterPro: IPR003594; ATPase.

DR InterPro: IPR004358; Bact_sens_pr_C.

DR InterPro: IPR003660; HAMP.

DR InterPro: IPR003661; His_kin.

DR InterPro: IPR004359; His_kin_sig.

DR InterPro: IPR001789; Response_reg.

DR Pfam: PF00672; HAMP; 1.

DR Pfam: PF02518; HATPase_C; 1.

DR Pfam: PF00072; Response_reg; 1.

DR Pfam: PF00512; signal; 1.

DR PRINTS: PR00344; BCTRLSENSOR.

DR PRODOM: PD000039; Response_reg; 1.

DR SMART: SM00304; HAMP; 1.

DR SMART: SM00387; HATPase_C; 1.

DR SMART: SM00388; HisKA; 1.

DR SMART: SM00448; REC; 1.

KW Kinase; Phosphorylation; Sensory transduction; Transferase;

KW Complete proteome.

SQ SEQUENCE 862 AA; 97846 MW; AB6814A3B63626C0 CRC64;

Query Match 2.0%; Score 9; DB 16; Length 862;

Best Local Similarity 100.0%; Pred. No. 3.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LSTLTLSTL 13

DB 293 LSTLTLSTL 301

RESULT 4

O9AX85 PRELIMINARY: PRT: 1432 AA.

AC 09AX85: 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Putative ABC transporter protein.

GN P0410E03.7.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Eriaristidae; Oryzaceae; Oryza.

OX NCBI_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIPPONBARE;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RA "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC

RT clone: P0410E03."

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AP002844; BAB21276.1;

DR InterPro: IPR003593; AAA_ATPase.

DR InterPro: IPR003439; ABC_transportr.

DR Pfam: PF00005; ABC_tran; 2.

DR PRODOM: PD000006; ABC_transportr; 1.

DR SMART: SM00382; AAA; 2.

KW ATP-binding.

SQ SEQUENCE 1432 AA; 160234 MW; 04E8CF2CA08D993 CRC64;

Query Match 2.0%; Score 9; DB 10; Length 1432;

Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 170 FTPLSLSD 178

DB 830 FTPLSLSD 838

RESULT 5

O8TUS3 PRELIMINARY: PRT: 227 AA.

AC 08TUS3: 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Predicted phosphatase of the PNP family.

GN MK1681.
 OS Methanopyrus kandleri.
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
 OC Methanopyrus.
 OX NCBI_TaxID=2320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AV19 / DSM 6324 / JCM 9639;
 RX MEDLINE=21927647; PubMed=11930014;
 RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
 RA Shcherbina O.V., Shakhova V.V., Belova G.I., Aravind L.,
 RA Natale D.A., Kogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
 RA Mal'kh A.G., Koonin E.V., Kozaykin S.A.;
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
 and monophyly of archaeal methanogens.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
 DR EMBL; AE010457; AAM02894.1; -
 KM Complete proteome.
 SQ SEQUENCE 227 AA; 24975 MW; B80099EE2BA8912 CRC64;

Query Match 1.8%; Score 8; DB 17; Length 227;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 LVHGETPA 112
 DB 106 LVHGETPA 113

RESULT 6
 O9M268 PRELIMINARY; PRT; 299 AA.
 AC O9M268;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE RAV-like protein.
 GN F21F14.140.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Choisme N., Robert C., Brottier P., Wincker P., Cattolico L.,
 RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X., Quettier F., Salanoubat M.;
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AL138642; CAB71904.1; -
 DR InterPro: IPR003340; TF_B3.
 DR Pfam: PF02362; B3; 1.
 SQ SEQUENCE 299 AA; 34270 MW; 2AB841F179DD174B CRC64;

Query Match 1.8%; Score 8; DB 10; Length 299;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 174 SLSFDLR 181
 DB 292 SLSFDLR 299

RESULT 7
 O9CI22 PRELIMINARY; PRT; 306 AA.
 AC O9CI22;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein PM1426.
 GN PM1426.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang O., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida PM70.";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL; AE006179; AK03510.1; -
 DR HSSP; P00631; 10D6.
 DR InterPro: IPR003187; PLA1.
 DR Pfam: PF02253; PLA1; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 306 AA; 35580 MW; EAF3DE8C1C22B26E CRC64;

Query Match 1.8%; Score 8; DB 16; Length 306;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 314 KLSRSMNR 321
 DB 184 KLSRSMNR 191

RESULT 8
 O94ZC0 PRELIMINARY; PRT; 415 AA.
 AC O94ZC0;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE NADH dehydrogenase subunit 2 (Fragment).
 GN NAD2.
 OS Isoetes duriei.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Lycophodophyta; Isoetopsida; Isoetales; Isoetaceae; Isoetes.
 OX NCBI_TaxID=56743;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Knopf V.;
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
 CC -1 CATALYTIC ACTIVITY: NADH + UBIOQUINONE - NAD(+) + UBIOQUINOL.
 DR EMBL; AJ409119; CAC50076.1; -
 DR InterPro: IPR001750; Oxidored_q1.
 DR InterPro: IPR003880; Pantine_attach.
 DR Pfam: PF00361; oxidored_q1; 1.
 DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
 KM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
 FT NON_TER 1
 FT 1
 SQ SEQUENCE 415 AA; 45082 MW; E0D3ACC7820F6309 CRC64;

Query Match 1.8%; Score 8; DB 8; Length 415;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LSTLTLSI 12
 DB 341 LSTLTLSI 348

RESULT 9
 O67608 PRELIMINARY; PRT; 55 AA.
 AC O67608;
 DT 067608

DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Tomato golden mosaic virus subgenomic DNA derived from DNA B ccdds -
DE covalently closed circular double-stranded molecule.
OS Tomato golden mosaic virus (TGMV).
OC Viruses; ssDNA viruses; Gemintviridae; Begomovirus.
OX NCBI_TaxID=10831;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87040767; PubMed=3022243;
RA MacDowell S.W., Courts R.H.A., Buck K.W.;
RT "Molecular characterization of subgenomic single-stranded and double-
RT stranded DNA forms isolated from plants infected with tomato golden
RT mosaic virus.";
RL Nucleic Acids Res. 14:7967-7984(1986).
DR EMBL; X04485; CAA28171.1; -;
DR InterPro: IPR000211; Gemint_BL.
DR Pfam: PF00845; Gemint_BL; 1.
SQ SEQUENCE 55 AA; 6281 MW; 41963570D739EC96 CRC64;

Query Match 1.6%; Score 7; DB 12; Length 55;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 312 SAKISRS 318
DB 43 SAKISRS 49

RESULT 10
ID Q92FV7 PRELIMINARY; PRT; 68 AA.
AC Q92FV7;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Hypothetical protein RC1370.
GN RC1370.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALISH 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Sanson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
DR EMBL; AE008682; AL03908.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 68 AA; 7373 MW; 9BF44F56AE4E8EC6 CRC64;

Query Match 1.6%; Score 7; DB 16; Length 68;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 TALENKT 84
DB 45 TALENKT 51

RESULT 11
ID Q91ZS4 PRELIMINARY; PRT; 72 AA.
AC Q91ZS4;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Coat protein (Fragment).

GN CP.
OC Potato virus Y strain NTN (PVY(NTN)).
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=122280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TUBER NECROSING;
RA Cerovska N., Filigaro M., Moravec T., Petrzik K.;
RT "Differences in nucleotide and amino acid sequences of N-terminal
RT parts of coat proteins among isolates of potato virus Y-NTN strain.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF228634; AAF67875.1; -;
DR InterPro: IPR001592; Poty_coat.
DR Pfam: PF00767; Poty_coat; 1.
FT NON_TER 1 1
FT NON_TER 72 72
SQ SEQUENCE 72 AA; 7692 MW; 4F129B870523B482 CRC64;

Query Match 1.6%; Score 7; DB 12; Length 72;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 156 TKKDAQ 162
DB 11 TKKDAQ 17

RESULT 12
ID Q91ZS5 PRELIMINARY; PRT; 72 AA.
AC Q91ZS5;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Coat protein (Fragment).
GN CP.
OS Potato virus Y strain NTN (PVY(NTN)).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=122280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TUBER NECROSING;
RA Cerovska N., Filigaro M., Moravec T., Petrzik K.;
RT "Differences in nucleotide and amino acid sequences of N-terminal
RT parts of coat proteins among isolates of potato virus Y-NTN strain.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF228633; AAF67874.1; -;
DR InterPro: IPR001592; Poty_coat.
DR Pfam: PF00767; Poty_coat; 1.
FT NON_TER 1 1
FT NON_TER 72 72
SQ SEQUENCE 72 AA; 7721 MW; 2C5287E15624CBDD CRC64;

Query Match 1.6%; Score 7; DB 12; Length 72;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 156 TKKDAQ 162
DB 11 TKKDAQ 17

RESULT 13
ID Q91ZS3 PRELIMINARY; PRT; 95 AA.
AC Q91ZS3;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Coat protein (Fragment).
GN CP.

```

OS   Potato virus Y strain NTN (PVY(NTN)).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OX   Polyvirus.
RN   NCBI_TaxID=122280;
RP   SEQUENCE FROM N.A.
RC   STRAIN=TUBER NECROSING;
RA   Cerovsky N., Filigayova M., Moravec T., Petrzik K.;
RT   "Differences in nucleotide and amino acid sequences of N-terminal
RL   parts of coat proteins among isolates of potato virus Y-NTN strain.";
DR   EMBL: AF228635; AAF67876.1; -.
DR   InterPro: IPR001592; Poly_coat.
DR   Pfam: PF00767; Poly_coat; 1.
FT   NON_TER 1
SQ   SEQUENCE 95 AA; 10446 MW; 28C06891777C9928 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 TKKDAQ 162
Db 11 TKKDAQ 17

RESULT 14
QY1ZS8
ID 091ZS8 PRELIMINARY; PRT; 96 AA.
AC 091ZS8;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Coat protein (Fragment).
GN CP.
OS Potato virus Y (strain N) (PVY).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Polyvirus.
OX NCBI_TaxID=12219;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NECROSING;
RA Cerovsky N., Filigayova M., Moravec T., Petrzik K.;
RT "Differences in nucleotide and amino acid sequences of N-terminal
RL parts of coat proteins among isolates of potato virus Y-NTN strain.";
DR EMBL: AF228630; AAF67871.1; -.
DR InterPro: IPR001592; Poly_coat.
DR Pfam: PF00767; Poly_coat; 1.
FT NON_TER 1
SQ SEQUENCE 96 AA; 10559 MW; 89C3A5675B9784CA CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 TKKDAQ 162
Db 11 TKKDAQ 17

RESULT 15
QY1Z148
ID 012148 PRELIMINARY; PRT; 100 AA.
AC 012148;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE ORF YDL163W.
GN YDL163W.
OS Saccharomyces cerevisiae (Baker's Yeast).

```

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OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pohl T.M.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   MIPS;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ALPHAS288C;
RA   Pohl T.M.;
RL   Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
DR   EMBL: Z74212; CAA98738.1; -.
DR   EMBL: Z67750; CAA91583.1; -.
DR   SGD: S0002322; YDL163W.
KW   Hypothetical protein.
SQ   SEQUENCE 100 AA; 10751 MW; 952FB92C852AA710 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 100;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LTLSTLS 14
Db 26 LTLSTLS 32

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Search completed: November 12, 2002, 11:48:24
 Job time : 27.25 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:40 : Search time 30 Seconds
(without alignments)
1963.226 Million cell updates/sec

Title: US-09-787-083-8

Perfect score: 442
Sequence: 1 MKVSLSTLTLSILPCFAILA.....YNHEATSPGVGLMLNDMWGL 442

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: A_Geneseq_101002:*

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21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	442	100.0	442	21	AAV85271
2	327	74.0	442	21	AAV85268
3	316	71.5	442	21	AAV85270
4	289	65.4	289	23	AAO17569
5	289	65.4	442	21	AAV85269
6	9	2.0	255	22	ABG18034
7	9	2.0	370	21	AAV75156
8	9	2.0	370	21	AAV75157
9	9	2.0	370	21	AAV75158
10	9	2.0	374	21	AAV70629

11	9	2.0	375	21	AAV70628
12	8	1.8	278	21	AAG11137
13	8	1.8	283	21	AAG11136
14	8	1.8	299	21	AAG11135
15	16	1.6	16	21	AAV85217
16	7	1.6	50	21	AAV79483
17	7	1.6	64	21	AAV85217
18	7	1.6	75	22	AAU22323
19	7	1.6	82	21	AAV85217
20	7	1.6	106	21	AAV85217
21	7	1.6	106	21	AAV85217
22	7	1.6	108	21	AAV85217
23	7	1.6	114	22	AAV85217
24	7	1.6	116	21	AAV85217
25	7	1.6	116	23	ABG65204
26	7	1.6	116	23	ABG65205
27	7	1.6	116	23	ABG65206
28	7	1.6	116	23	AAU91093
29	7	1.6	116	23	AAU91120
30	7	1.6	116	23	AAU91121
31	7	1.6	133	22	ABG27556
32	7	1.6	136	21	AAV85217
33	7	1.6	158	21	AAV79176
34	7	1.6	162	23	ABP42371
35	7	1.6	169	20	AAV34661
36	7	1.6	181	21	AAV37809
37	7	1.6	181	23	ABP42926
38	7	1.6	186	21	AAV85217
39	7	1.6	186	21	AAV85217
40	7	1.6	188	21	AAV85217
41	7	1.6	190	21	AAV85217
42	7	1.6	214	22	ABG65814
43	7	1.6	221	23	ABG68103
44	7	1.6	256	22	AAU25462
45	7	1.6	268	13	AAV21542

ALIGNMENTS

RESULT 1	AAV85271	standard; Protein; 442 AA.
ID	AAV85271	
AC	AAV85271	
DT	29-JUN-2000	(first entry)
DE	BASB034 amino acid sequence #4.	
KW	Moraxella catarrhalis infection; BASB034; diagnosis; staging;	
KW	vaccine; bacteriostatic; treatment; prevention; otitis media;	
KW	sinusitis; nosocomial infection; invasive disease; chronic otitis media;	
KW	hearing loss; antibacterial drug.	
OS	Moraxella catarrhalis.	
PN	WO200015802-A1.	
PD	23-MAR-2000.	
PF	14-SEP-1999;	99WO-EP06781.
PR	14-SEP-1998;	98GB-0020002.
PA	(SMK) SMITHKLINE BEECHAM BIOLOGICALS.	
PI	Ruelle J;	
DR	WPI; 2000-271440/23.	
DR	N-PSDB; AAA10703.	
XX	Novel BASB034 polynucleotides and polypeptides from Moraxella	

PT catarrhals used to prepare vaccines against bacterial infections -
XX
PS Claim 3; Page 69; 106pp; English.
XX
CC This sequence represents a Moraxella catarrhals BASB034 polypeptide from
CC strain Mc2969. The invention relates to BASB034 polypeptides from
CC M. catarrhals strains Mc2931, Mc2908, Mc2913 and Mc2969. The BASB034
CC polynucleotides and polypeptides may be employed as research reagents and
CC material for the discovery of treatments and diagnostics for diseases,
CC particularly human diseases. They are particularly used to diagnose and
CC treat M. catarrhals infections. They can be used for diagnosis of
CC disease, staging of disease, or determining response of an infectious
CC organism to drugs. The polynucleotides may be used as a source for
CC hybridization probes, and for screening of genetic mutations, serotype,
CC organism or strain identification, identification of mutations in BASB034
CC sequences, and as components of arrays which are useful for diagnostic
CC and prognostic purposes. The polypeptides can be used to produce
CC antibodies. The polypeptides can also be used in vaccine formulations,
CC and to identify agonists and antagonists. The polypeptides, antibodies,
CC agonists and antagonists (which are bacteriostatic) are used for the
CC treatment and prevention of diseases such as otitis media in infants and
CC children, pneumonia in elderlies, sinusitis, nosocomial infections and
CC invasive diseases, and chronic otitis media with hearing loss. The
CC polypeptides, agonists and antagonists are also used for screening of
CC antibacterial drugs. The BASB034 products of the invention can be used
CC screen for new antibacterial compounds that may target resistant
CC bacteria.
XX
SQ Sequence 442 AA;
Query Match 100.0%; Score 442; DB 21; Length 442;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKVSLSTLTSLILPCFALIAIQQAQAVNPVAFVDEVRSENDLGQDNELPIDVQASQTOSA 60
Db 1 MKVSLSTLTSLILPCFALIAIQQAQAVNPVAFVDEVRSENDLGQDNELPIDVQASQTOSA 60
QY 61 STDANPDEHEPELYTALLENKTMILNCSALNODIMRLACYDTLVHGEPYAVIKTKRSI 120
Db 61 STDANPDEHEPELYTALLENKTMILNCSALNODIMRLACYDTLVHGEPYAVIKTKRSI 120
QY 121 RLDETIMOTIKGPOVVOYQETTDPIFLMGNEKGMILTKDAKOLEYAAKQFTPLSFDLD 180
Db 121 RLDETIMOTIKGPOVVOYQETTDPIFLMGNEKGMILTKDAKOLEYAAKQFTPLSFDLD 180
QY 121 RLDETIMOTIKGPOVVOYQETTDPIFLMGNEKGMILTKDAKOLEYAAKQFTPLSFDLD 180
Db 121 RLDETIMOTIKGPOVVOYQETTDPIFLMGNEKGMILTKDAKOLEYAAKQFTPLSFDLD 180
QY 181 RNNTPPLMSSRPHPNPYVLPPIFMHGKPNRSPNTPSHEAKQFTPNERRAPELKQVSVKXKA 240
Db 181 RNNTPPLMSSRPHPNPYVLPPIFMHGKPNRSPNTPSHEAKQFTPNERRAPELKQVSVKXKA 240
QY 241 AEDLMGTDSDLMFEGYTOOSHQIFNGKNSRPPRVNDYQPEITFLQPYTSDLPMDGKVRMI 300
Db 241 AEDLMGTDSDLMFEGYTOOSHQIFNGKNSRPPRVNDYQPEITFLQPYTSDLPMDGKVRMI 300
QY 241 AEDLMGTDSDLMFEGYTOOSHQIFNGKNSRPPRVNDYQPEITFLQPYTSDLPMDGKVRMI 300
Db 241 AEDLMGTDSDLMFEGYTOOSHQIFNGKNSRPPRVNDYQPEITFLQPYTSDLPMDGKVRMI 300
QY 301 GMGAVHHSNGSBAKLSRSMNRAYLWAGMEKNTLVNPRIMGRIFEGSGSOPDDNDPDLTD 360
Db 301 GMGAVHHSNGSBAKLSRSMNRAYLWAGMEKNTLVNPRIMGRIFEGSGSOPDDNDPDLTD 360
QY 361 YYGADVAFELQLENKNSISGTVRNPRSGKALQLDVYVPLGKIGISYFOIFQSGQSL 420
Db 361 YYGADVAFELQLENKNSISGTVRNPRSGKALQLDVYVPLGKIGISYFOIFQSGQSL 420
QY 421 IDYNHEATSFSGVGLMLNDMGL 442
Db 421 IDYNHEATSFSGVGLMLNDMGL 442
RESULT 2
AAV85268 ID AAV85268 standard; Protein: 442 AA.
XX
AC AAV85268;
XX

DT 29-JUN-2000 (first entry)
XX
DE BASB034 amino acid sequence #1.
XX
KW Moraxella catarrhals infection; BASB034; diagnosis; staging;
KW vaccine; bacteriostatic; treatment; prevention; otitis media; pneumonia;
KW sinusitis; nosocomial infection; invasive disease; chronic otitis media;
KW hearing loss; antibacterial drug.
XX
OS Moraxella catarrhals.
XX
PM WO200015802-A1.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-EP06781.
XX
PR 14-SEP-1998; 98GB-0020002.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Ruelle J;
XX
DR WPI: 2000-271440/23.
DR N-PSDB; AAA10700.
XX
PT Novel BASB034 polynucleotides and polypeptides from Moraxella
XX catarrhals used to prepare vaccines against bacterial infections -
PS Claim 3; Fig 2; 106pp; English.
XX
CC This sequence represents a Moraxella catarrhals BASB034 polypeptide from
CC strain Mc2931 (ATCC 43617). The invention relates to BASB034 polypeptides
CC from M. catarrhals strains Mc2931, Mc2908, Mc2913 and Mc2969. The
CC BASB034 polynucleotides and polypeptides may be employed as research
CC reagents and material for the discovery of treatments and diagnostics for
CC diseases, particularly human diseases. They are particularly used to
CC diagnose and treat M. catarrhals infections. They can be used for
CC diagnosis of disease, staging of disease, or determining response of an
CC infectious organism to drugs. The polynucleotides may be used as a source
CC for hybridization probes, and for screening of genetic mutations,
CC serotype, organism or strain identification, identification of mutations
CC in BASB034 sequences, and as components of arrays which are useful for
CC diagnostic and prognostic purposes. The polypeptides can be used to
CC produce antibodies. The polypeptides can also be used in vaccine
CC formulations, and to identify agonists and antagonists. The polypeptides,
CC antibodies, agonists and antagonists (which are bacteriostatic) are used
CC for the treatment and prevention of diseases such as otitis media in
CC infants and children, pneumonia in elderlies, sinusitis, nosocomial
CC infections and invasive diseases, and chronic otitis media with hearing
CC loss. The polypeptides, agonists and antagonists are also used for
CC screening of antibacterial drugs. The BASB034 products of the invention
CC can be used screen for new antibacterial compounds that may target
CC resistant bacteria.
XX
SQ Sequence 442 AA;
Query Match 74.0%; Score 327; DB 21; Length 442;
Best Local Similarity 99.8%; Pred. NO. 4.3e-309;
Matches 427; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 CFALLAIQQAQAVNPVAFVDEVRSENDLGQDNELPIDVQASQTOSAFTDANPDEHEPE 74
Db 15 CFALLAIQQAQAVNPVAFVDEVRSENDLGQDNELPIDVQASQTOSAFTDANPDEHEPE 74
QY 75 LYTTALENKTMLNCSALNODIMRLACYDTLVHGEPYAVIKTKRSIRDETIMOTIKGP 134
Db 75 LYTTALENKTMLNCSALNODIMRLACYDTLVHGEPYAVIKTKRSIRDETIMOTIKGP 134
QY 135 OVVOYQETTDPIFLMGNEKGMILTKDAKOLEYAAKQFTPLSFDLDRNNTPLMSSRPHPNP 194
Db 135 OVVOYQETTDPIFLMGNEKGMILTKDAKOLEYAAKQFTPLSFDLDRNNTPLMSSRPHPNP 194

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QY 195 MYVLPFIMHGKPNRSPNTPSHAKOFTPNFPAPELKFQVSVYKAAEDLMGTDSDLMFG 254
DB 195 MYVLPFIMHGKPNRSPNTPSHAKOFTPNFPAPELKFQVSVYKAAEDLMGTDSDLMFG 254
QY 255 YTGQSHMOIFNGKNSRPFVHDYQPEIFLTQPVYSDLPMDGKVRMIGAVHNSGESAK 314
DB 255 YTGQSHMOIFNGKNSRPFVHDYQPEIFLTQPVYSDLPMDGKVRMIGAVHNSGESAK 314
QY 315 LSRSMNRAVLMAGMEKMLTVMPRIWGRIFKEGSGSQPDNDPDIIDYGYGDFRFLYOLE 374
DB 315 LSRSMNRAVLMAGMEKMLTVMPRIWGRIFKEGSGSQPDNDPDIIDYGYGDFRFLYOLE 374
QY 375 NKSNTISGVRRNPNRSGKALQLDYVYPLGKIGISGFQIFQGYGQSLIDYNHEATSEFGVL 434
DB 375 NKSNTISGVRRNPNRSGKALQLDYVYPLGKIGISGFQIFQGYGQSLIDYNHEATSEFGVL 434
QY 435 MLNDMGL 442
DB 435 MLNDMGL 442

RESULT 3
AAY85270
ID AAY85270 standard; Protein: 442 AA.
AC AAY85270;
XX 29-JUN-2000 (first entry)
DE BASB034 amino acid sequence #3.
XX
KW Moraxella catarrhalis infection; BASB034; diagnosis; staging;
KW vaccine; bacteriostatic; treatment; prevention; otitis media; pneumonia;
KW sinusitis; nosocomial infection; invasive disease; chronic otitis media;
KW hearing loss; antibacterial drug.
XX
OS Moraxella catarrhalis.
XX
FN MO200015802-A1.
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-EP06781.
XX
PR 14-SEP-1999; 98GB-0020002.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Ruelle J;
XX
DR WPI: 2000-271440/23.
XX
DR N-PSDB; AAA10702.
XX
PT Novel BASB034 polynucleotides and polypeptides from Moraxella
XX catarrhalis used to prepare vaccines against bacterial infections
XX
PS Claim 3; Page 68; 106pp; English.
XX
XX This sequence represents a Moraxella catarrhalis BASB034 polypeptide from
XX strain Mc2913. The invention relates to BASB034 polypeptides from
XX M. catarrhalis strains Mc2913, Mc2908, Mc2913 and Mc2969. The BASB034
XX polynucleotides and polypeptides may be employed as research reagents and
XX material for the discovery of treatments and diagnostics for diseases,
XX particularly human diseases. They are particularly used to diagnose and
XX treat M. catarrhalis infections. They can be used for diagnosis of
XX disease, staging of disease, or determining response of an infectious
XX organism to drugs. The polynucleotides may be used as a source for
XX hybridization probes, and for screening of genetic mutations, serotype,
XX organism or strain identification, identification of mutations in BASB034
XX sequences, and as components of arrays which are useful for diagnostic
XX and prognostic purposes. The polypeptides can be used to produce
XX antibodies. The polypeptides can also be used in vaccine formulations,
XX and to identify agonists and antagonists. The polypeptides, antibodies,

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CC agonists and antagonists (which are bacteriostatic) are used for the
CC treatment and prevention of diseases such as otitis media in infants and
CC children, pneumonia in elders, sinusitis, nosocomial infections and
CC invasive diseases, and chronic otitis media with hearing loss. The
CC polypeptides, agonists and antagonists are also used for screening of
CC antibacterial drugs. The BASB034 products of the invention can be used
CC screen for new antibacterial compounds that may target resistant
CC bacteria.
XX
SQ Sequence 442 AA:
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Query Match 71.5%; Score 316; DB 21; Length 442;
Best Local Similarity 99.8%; Pred. No. 2,1e-298;
Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 26 AVPNPVAFAFDEVSRSENDLGQDNELPIDVQASATQASTDPANPLDEHEPELYTALENKTM 85
QY 86 LINCASALNODIMRLACYPDTLVHGETPVAIKTKRSIRLDETTWQTTKGRQVYYQETTDPI 145
DB 86 LINCASALNODIMRLACYPDTLVHGETPVAIKTKRSIRLDETTWQTTKGRQVYYQETTDPI 145
QY 146 FLMGNEKGM/LTKKDAKOLEYAKOFTPLSLSPDLRNNTPMLSSRPHNPMYVLPFIMHGK 205
DB 146 FLMGNEKGM/LTKKDAKOLEYAKOFTPLSLSPDLRNNTPMLSSRPHNPMYVLPFIMHGK 205
QY 206 PNRSPNTPSHAKOFTPNFPAPELKFQVSVYKAAEDLMGTDSDLMFGYTGQSHMOIFN 265
DB 206 PNRSPNTPSHAKOFTPNFPAPELKFQVSVYKAAEDLMGTDSDLMFGYTGQSHMOIFN 265
QY 266 GKNRSPFRVHDYQPEIFLTQPVYSDLPMDGKVRMIGAVHNSGESAKLSMNRAYLM 325
DB 266 GKNRSPFRVHDYQPEIFLTQPVYSDLPMDGKVRMIGAVHNSGESAKLSMNRAYLM 325
QY 326 AGMEKMLTVMPRIWGRIFKEGSGSQPDNDPDIIDYGYGDFRFLYOLENKNISGVTRY 385
DB 326 AGMEKMLTVMPRIWGRIFKEGSGSQPDNDPDIIDYGYGDFRFLYOLENKNISGVTRY 385
QY 386 NPSRSGKALQLDYVYPLGKIGISGFQIFQGYGQSLIDYNHEATSEFGVGLMLNDMGL 442
DB 386 NPSRSGKALQLDYVYPLGKIGISGFQIFQGYGQSLIDYNHEATSEFGVGLMLNDMGL 442

RESULT 4
AAO17569
ID AAO17569 standard; Protein: 289 AA.
XX
AC AAO17569;
XX
DT 19-JUL-2002 (first entry)
XX
DE M catarrhalis MCA100712 protein SEQ ID NO: 18.
XX
KW Moraxella; vaccine; respiratory tract infection; antiinflammatory;
KW auditory; antibacterial; otitis media; sinusitis; pneumonia.
XX
XX Moraxella catarrhalis.
XX
OS
XX
FN MO200218595-A2.
XX
PD 07-MAR-2002.
XX
XX 28-AUG-2001; 2001WO-CA01221.
XX
XX 28-AUG-2000; 2000US-228294P.
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XX 28-AUG-2000; 2000US-228295P.
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XX 28-AUG-2000; 2000US-228296P.
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XX 29-AUG-2000; 2000US-228438P.
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XX 29-AUG-2000; 2000US-228439P.
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XX 29-AUG-2000; 2000US-228440P.
XX
XX 29-AUG-2000; 2000US-228441P.
XX
XX 29-AUG-2000; 2000US-228442P.

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PR 29-AUG-2000; 2000US-228443P.
PR 29-AUG-2000; 2000US-228511P.
PR 29-AUG-2000; 2000US-228512P.
PR 29-AUG-2000; 2000US-228742P.
PR 29-AUG-2000; 2000US-228773P.
PR 01-SEP-2000; 2000US-229465P.
PR 01-SEP-2000; 2000US-229474P.
PR 01-SEP-2000; 2000US-229475P.
PR 01-SEP-2000; 2000US-229478P.
PR 05-SEP-2000; 2000US-229740P.
PR 05-SEP-2000; 2000US-229803P.
PR 05-SEP-2000; 2000US-229804P.
PR 05-SEP-2000; 2000US-229805P.
PR 05-SEP-2000; 2000US-229806P.
PR 05-SEP-2000; 2000US-229809P.
PR 05-SEP-2000; 2000US-229811P.
PR 06-SEP-2000; 2000US-230214P.
PR 06-SEP-2000; 2000US-230250P.
PR 06-SEP-2000; 2000US-230252P.
XX
XX (AVENTIS PASTEUR LTD.
XX
XX Loosmore S, Wang J, Bradley B, Ochs M, Yang Y;
XX
XX WPI: 2002-401721/43.
XX
XX N-PSDB; AAL46501.
XX
XX Moraxella polypeptide and polynucleotides useful as vaccine for
XX immunizing a host e.g. humans against disease e.g. otitis media,
XX pneumonia, caused by infection of the bacteria
XX
XX
XX Claim 26; Fig 17; 277pp; English.
XX
XX The present invention provides the protein and coding sequences of
XX CC proteins from Moraxella catarrhalis. These can be used to produce
XX CC vaccines which protect against M. catarrhalis infection, which can cause
XX CC otitis media, respiratory infection, sinusitis, and pneumonia. The
XX CC present sequence is a protein of the invention.
XX
XX
XX Sequence 289 AA;
SQ
Query Match 65.4%; Score 289; DB 23; Length 289;
Best Local Similarity 100.0%; Pred. No. 2.5e-272;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLETKDAKOLEYAKOFTPLSLSFDDLRNNTPLMSSRPHNPMYVLPJFMHGKPNRSPPTP 60
QY 214 SHEAKOFTPNFEFRAPBELKFOYSVKVKAEDLMGTDSDLMFGYTOQSHWQIFNGKNSRPF 273
DB 61 SHEAKOFTPNFEFRAPBELKFOYSVKVKAEDLMGTDSDLMFGYTOQSHWQIFNGKNSRPF 120
QY 274 VHDQPEIFLTPQPYSDLPMDGKVRMTGMGVHNSNGESAKLSNMRAYLMAEMKNTL 333
DB 121 VHDQPEIFLTPQPYSDLPMDGKVRMTGMGVHNSNGESAKLSNMRAYLMAEMKNTL 180
QY 334 TVMPRIWGRITKEGSGSQPDNDPILDYGYGADVRFYQLEKNKSNISGTAVYNRSGKA 393
DB 181 TVMPRIWGRITKEGSGSQPDNDPILDYGYGADVRFYQLEKNKSNISGTAVYNRSGKA 240
QY 394 LQDDYVPLGKISGYFOIFQGYGOSLIDYVNEHTSFGVGIMLDMKGL 442
DB 241 LQDDYVPLGKISGYFOIFQGYGOSLIDYVNEHTSFGVGIMLDMKGL 289
RESULT 5
AA185269
ID AAY85269 standard; Protein; 442 AA.
AC AAY85269;
XX
XX 29-JUN-2000 (first entry)
```

```
XX BASB034 amino acid sequence #2.
DE
XX Moraxella catarrhalis infection; BASB034; diagnosis; staging;
XX vaccine; bacteriostatic; treatment; prevention; otitis media; pneumonia;
XX sinusitis; nosocomial infection; invasive disease; chronic otitis media;
XX hearing loss; antibacterial drug.
XX
XX Moraxella catarrhalis.
OS
XX WO200015802-A1.
XX
XX 23-MAR-2000.
PD
XX
XX 14-SEP-1999; 99WO-EP06781.
XX
XX 14-SEP-1998; 98GB-0020002.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Ruelle J;
XX
XX WPI: 2000-271440/23.
XX
XX N-PSDB; AAL10701.
XX
XX Novel BASB034 polynucleotides and polypeptides from Moraxella
XX catarrhalis used to prepare vaccines against bacterial infections
XX
XX Claim 3; Page 67; 106pp; English.
XX
XX This sequence represents a Moraxella catarrhalis BASB034 polypeptide from
XX CC strain Mc2908. The invention relates to BASB034 polypeptides from
XX CC M. catarrhalis strains Mc2931, Mc2908, Mc2913 and Mc2969. The BASB034
XX CC polynucleotides and polypeptides may be employed as research reagents and
XX CC material for the discovery of treatments and diagnostics for diseases,
XX CC particularly human diseases. They are particularly used to diagnose and
XX CC treat M. catarrhalis infections. They can be used for diagnosis of
XX CC disease, staging of disease, or determining response of an infectious
XX CC organism to drugs. The polynucleotides may be used as a source for
XX CC hybridization probes, and for screening of genetic mutations, serotype,
XX CC organism or strain identification, identification of mutations in BASB034
XX CC sequences, and as components of arrays which are useful for diagnostic
XX CC and prognostic purposes. The polypeptides can be used to produce
XX CC antibodies. The polypeptides can also be used in vaccine formulations,
XX CC and to identify agonists and antagonists. The polypeptides, antibodies,
XX CC agonists and antagonists (which are bacteriostatic) are used for the
XX CC treatment and prevention of diseases such as otitis media in infants and
XX CC children, pneumonia in elderlies, sinusitis, nosocomial infections and
XX CC invasive diseases, and chronic otitis media with hearing loss. The
XX CC polypeptides, agonists and antagonists are also used for screening of
XX CC antibacterial drugs. The BASB034 products of the invention can be used
XX CC screen for new antibacterial compounds that may target resistant
XX CC bacteria.
XX
XX Sequence 442 AA;
SQ
Query Match 65.4%; Score 289; DB 21; Length 442;
Best Local Similarity 99.7%; Pred. No. 3.6e-272;
Matches 389; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 53 VQASATQASATDTANPLDHEPELYTTALENKTMILNCSALMODIMRLACYDTLVHGETPA 112
DB 53 VQASATQASATDTANPLDHEPELYTTALENKTMILNCSALMODIMRLACYDTLVHGETPA 112
QY 113 VIKTRSRIRLDETITWQITKGKQVNVYQETDPIFLMGNEKGLTKKAKOLEYAKOFTP 172
DB 113 VIKTRSRIRLDETITWQITKGKQVNVYQETDPIFLMGNEKGLTKKAKOLEYAKOFTP 172
QY 173 LSLSFDDLRNNTPLMSSRPHNPMYVLPJFMHGKPNRSPPTSHAKOFTPNFEFRAPBELKF 232
DB 173 LSLSFDDLRNNTPLMSSRPHNPMYVLPJFMHGKPNRSPPTSHAKOFTPNFEFRAPBELKF 232
QY 233 QVSVKRAEDLMGTDSDLMFGYTOQSHWQIFNGKNSRPFVNDYDPEIFLTPQVSDLP 292
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|||||
 DB 233 QVSKVAAEDLWGTTSDLFQITQDSHMOIFNGKNSRPRVMDYQPEIFLTQPVYSDLP 292
 QY 293 WDGKVRMIGMAVHSHNGESAKLSRSWNRAYLWAGMEMKNTVPRIWGRIFKSGSOP 352
 DB 293 WDGKVRMIGMAVHSHNGESAKLSRSWNRAYLWAGMEMKNTVPRIWGRIFKSGSOP 352
 QY 353 DDNPDIIDYGYGVDYRLYOLENKSNTSGTVRNPBSGKALQIDYVPLGKIGSYFOI 412
 DB 353 DDNPDIIDYGYGVDYRLYOLENKSNTSGTVRNPBSGKALQIDYVPLGKIGSYFOI 412
 QY 413 FQGYGSLIDYNHEATSEGVGLMIDMGL 442
 DB 413 FQGYGSLIDYNHEATSEGVGLMIDMGL 442

RESULT 6
 ABG18034
 ID ABG18034 standard; Protein; 255 AA.
 AC ABG18034;
 DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #18025.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW Food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001WO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PA (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT.
 DR WPI, 2001-639362/73.
 DR N-PSDB; AAS82221.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS Claim 20: SEQ ID NO 48393; 103bp; English.
 XX
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (II) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 XX
 XX Sequence 255 AA;
 QY Query Match 2.0%; Score 9; DB 22; Length 255;
 DB Best Local Similarity 100.0%; Pred. No. 2.8;
 DB Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 279 PEIFLTQPV 287
 DB 204 PEIFLTQPV 212

RESULT 7
 AA75156
 ID AA75156 standard; Protein; 370 AA.
 AC AA75156;
 DT 21-MAR-2000 (first entry)
 DE Neisseria gonorrhoeae ORF 582 protein sequence SEQ ID NO:1786.
 KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
 KW antibacterial; gene therapy.
 OS Neisseria gonorrhoeae.
 PN WO9957280-A2.
 PD 11-NOV-1999.
 PF 30-APR-1999; 99WO-US09346.
 PR 01-MAY-1998; 98US-0083758.
 PR 31-JUL-1998; 98US-0094869.
 PR 02-SEP-1998; 98US-0098994.
 PR 02-SEP-1998; 98US-0099062.
 PR 09-OCT-1998; 98US-0103749.
 PR 09-OCT-1998; 98US-0103794.
 PR 09-OCT-1998; 98US-0103796.
 PR 25-FEB-1999; 99US-0121528.
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 PI Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;
 PI Petersen J, Piza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
 PI Tettelin H, Venter JC.
 DR WPI; 2000-062150/05.
 DR N-PSDB; AA253918.
 XX
 XX Claim 2: Page 903; 1453bp; English.
 CC AA253015 to AA254536, AA254577 to AA254615, and AA74253 to AA75941
 CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of
 CC the invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the
 CC manufacture of medicaments for treating or preventing infection due to
 CC Neisseria bacteria (e.g. meningitis and septicaemia), to detect the
 CC presence of Neisseria bacteria, or to raise antibodies. They may also
 CC be used to screen for agonists or antagonists, which may themselves
 CC have use as antibacterial agents. The polynucleotides of the invention
 CC may also be used in gene therapy protocols.

```
XX Sequence 370 AA:
SQ
Query Match 2.0%; Score 9; DB 21; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 279 PEIFLTQPV 287
Db 209 PEIFLTQPV 217
|||||
RESULT 8
AAV75157
ID AAV75157 standard; Protein; 370 AA.
XX
AC AAV75157;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 582 protein sequence SEQ ID NO:1788.
XX
KM Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
XX antibacterial; gene therapy.
OS Neisseria meningitidis.
XX
PN WO957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI: 2000-062150/05.
DR N-PSDB; AA253919.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics -
XX
PS Claim 2; Page 904; 1453pp; English.
XX
AA253015 to AA254536, AA254577 to AA254615, and AAV74253 to AAV75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC presence of Neisseria (e.g. meningitis and septicemia), to detect the
CC presence of Neisseria bacteria, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
SQ Sequence 370 AA;
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Query Match 2.0%; Score 9; DB 21; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 279 PEIFLTQPV 287
Db 209 PEIFLTQPV 217
|||||
RESULT 9
AAV75158
ID AAV75158 standard; Protein; 370 AA.
XX
AC AAV75158;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 582 protein sequence SEQ ID NO:1790.
XX
KM Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
XX antibacterial; gene therapy.
OS Neisseria meningitidis.
XX
PN WO957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI: 2000-062150/05.
DR N-PSDB; AA253920.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics -
XX
PS Claim 2; Page 905; 1453pp; English.
XX
AA253015 to AA254536, AA254577 to AA254615, and AAV74253 to AAV75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC presence of Neisseria (e.g. meningitis and septicemia), to detect the
CC presence of Neisseria bacteria, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
SQ Sequence 370 AA;
```

Query Match

2.0%; Score 9; DB 21; Length 370;

Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 PEIFLTQPV 287
|||||
DB 209 PEIFLTQPV 217

RESULT 10

AAV70629 standard; Protein; 374 AA.

AAV70629;

18-JUL-2000 (first entry)

Neisseria meningitidis serogroup B strain H44/76 BASB033 protein.

BASB033; diagnosis, prophylaxis; treatment; antibacterial; vaccine;

Neisseria meningitidis infection.

Neisseria meningitidis.

WO200015801-A1.

23-MAR-2000.

09-SEP-1999; 99WO-EP06718.

14-SEP-1998; 98GB-0020003.

(SMK) SMITHKLINE BEECHAM BIOLOGICALS.

Ruelle J;

WPI; 2000-271439/23.

N-PSDB; AA252134.

Isolated BASB033 polypeptides and polynucleotides of Neisseria

meningitidis, useful for diagnosis, prophylaxis and treatment of N.

meningitidis infection -

Claim 4; Page 59; 93pp; English.

The present sequence is a BASB033 protein from

Neisseria meningitidis serogroup B strain H44/76. The protein

shows homology to the Klebsiella pneumoniae outer membrane

phospholipase A. The present sequence is useful for diagnosis,

prophylaxis and treatment of N. meningitidis infection. It may also be

used for the discovery and development of antibacterial compounds and

in vaccine compositions.

Sequence 374 AA;

Query Match 2.0%; Score 9; DB 21; Length 374;

Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 PEIFLTQPV 287
|||||
DB 213 PEIFLTQPV 221

RESULT 11

AAV70628 standard; Protein; 375 AA.

AAV70628;

18-JUL-2000 (first entry)

Neisseria meningitidis serogroup B strain ATCC13090 BASB033 protein.

BASB033; diagnosis, prophylaxis; treatment; antibacterial; vaccine;
Neisseria meningitidis infection.

Neisseria meningitidis.

WO200015801-A1.

23-MAR-2000.

09-SEP-1999; 99WO-EP06718.

14-SEP-1998; 98GB-0020003.

(SMK) SMITHKLINE BEECHAM BIOLOGICALS.

Ruelle J;

WPI; 2000-271439/23.

N-PSDB; AA252133.

Isolated BASB033 polypeptides and polynucleotides of Neisseria

meningitidis, useful for diagnosis, prophylaxis and treatment of N.

meningitidis infection -

Claim 4; Page 58; 93pp; English.

The present sequence is a BASB033 protein from

Neisseria meningitidis serogroup B strain ATCC13090. The protein

shows homology to the Klebsiella pneumoniae outer membrane

phospholipase A. The present sequence is useful for diagnosis,

prophylaxis and treatment of N. meningitidis infection. It may also be

used for the discovery and development of antibacterial compounds and

in vaccine compositions.

Sequence 375 AA;

RESULT 12

AAG11137 standard; Protein; 278 AA.

AAG11137;

17-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 9741.

Protein identification; signal transduction pathway; metabolic pathway;

hybridisation assay; genetic mapping; gene expression control; promoter;

termination sequence.

Arabidopsis thaliana.

EPI033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

25-FEB-1999; 99US-0121825.

05-MAR-1999; 99US-0123180.

09-MAR-1999; 99US-0123548.

23-MAR-1999; 99US-0125788.

25-MAR-1999; 99US-0126264.

29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130044.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 21-JUN-1999; 99US-0139763.
PR 22-JUN-1999; 99US-0139817.
PR 23-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140693.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142053.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 23-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147202.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0153363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158223.
PR 12-OCT-1999; 99US-0158369.

PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
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PR 28-OCT-1999; 99US-0161993.
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 271 SLSEFDLDR 278

RESULT 13
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ID AG11136 standard; Protein; 283 AA.

XX AG11136;

DF 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 9740.

XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 1.8%; Score 8; DB 21; Length 283;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 174 SLSPFLDR 181
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Db 276 SLSPFLDR 283

RESULT 14

AAG1135 standard; Protein; 299 AA.

XX AAG1135;

XX AC AAG1135;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 9739.

XX KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.

PN EPI033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123160.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

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PR 29-OCT-1999; 99US-0162142.

Query Match 1.8%; Score 8; DB 21; Length 299;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 174 SLSPDLDR 181
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Db 292 SLSPDLDR 299

RESULT 15
AAR52127
ID AAR52127 standard; Peptide; 16 AA.

AC AAR52127;

DT 27-SEP-1996 (first entry)

DE Mouse light chain surface patch S03410.

KW antibody; humanised; murine; human; heavy chain; light; variable;
framework region; complementarity determining region; reshaping;
modelling; surface residue; modify.

OS Mus sp.

PN EP592106-A1.

PD 13-APR-1994.

PF 07-SEP-1993; 93EP-0307051.

PR 09-SEP-1992; 92US-0942245.

PA (PEDE/) PEDERSEN J T.
PA (IMMU-) IMMUNOGEN INC.

PI Gullid BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;

DR WPI; 1994-120230/15.

PT Method of resurfacing of rodent antibodies to produce humanised
antibody forms - for producing non-human antibodies with improved
therapeutic efficiency by presenting human surface on V-region

PS Example 1; Page 14; 230pp: English.

XX Modification of a rodent antibody or fragment by resurfacing in order
CC to produce a humanised rodent antibody can be determined by calculating
CC homology between murine and human antibody surfaces. In order to test
CC the resurfacing approach of the invention, three humanisation
CC experiments were set up. (1) traditional loop grafting; (2) resurfacing
CC approach using most similar chain; and (3) resurfacing approach using
CC human sequences with most similar surface residues. AAR52069-159 are the
CC surface residue patterns in mouse light chain antibody variable regions.
CC These "patches" were used in the third method, where rodent light and
CC heavy chains were matched and the most similar human sequence found
CC independently only over the surface residues indicated in AAR52030-67.
XX

SQ Sequence 16 AA;

Query Match 1.6%; Score 7; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 387 PRSGKA 393
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Db 4 PRSGKA 10

Search completed: November 12, 2002, 11:44:53
Job time : 31 secs

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OS Potato virus Y strain NTN (PVY(NTN)).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=122280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TUBER NECROSING;
RA Cerovska N., Filigiarova M., Moravec T., Petrzik K.;
RT "Differences in nucleotide and amino acid sequences of N-terminal
  parts of coat proteins among isolates of potato virus Y-NTN strain.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF228635; AA67876.1; -
DR InterPro: IPR001592; Poly_coat.
DR Pfam: PF00767; Poly_coat; 1.
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DB 11 TKDAKQ 17

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AC Q91ZS8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Coat protein (Fragment).
GN CP.
OS Potato virus Y (strain N) (PVY).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=12219;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NECROSING;
RA Cerovska N., Filigiarova M., Moravec T., Petrzik K.;
RT "Differences in nucleotide and amino acid sequences of N-terminal
  parts of coat proteins among isolates of potato virus Y-NTN strain.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF228630; AA67871.1; -
DR InterPro: IPR001592; Poly_coat.
DR Pfam: PF00767; Poly_coat; 1.
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SQ SEQUENCE 96 AA: 10559 MW: 89C3A5675B9784CA CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 TKDAKQ 162
DB 11 TKDAKQ 17

RESULT 15
Q91ZS6
ID Q91ZS6 PRELIMINARY; PRT; 101 AA.
AC Q91ZS6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Coat protein (Fragment).
GN CP.
OS Potato virus Y strain NTN (PVY(NTN)).

```

```

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=122280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TUBER NECROSING;
RA Cerovska N., Filigiarova M., Moravec T., Petrzik K.;
RT "Differences in nucleotide and amino acid sequences of N-terminal
  parts of coat proteins among isolates of potato virus Y-NTN strain.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF228632; AA67873.1; -
DR InterPro: IPR001592; Poly_coat.
DR Pfam: PF00767; Poly_coat; 1.
FT NON_TER 1 1
FT NON_TER 101 101
SQ SEQUENCE 101 AA: 11112 MW: B55BF51C3D5FE9BD CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 101;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 TKDAKQ 162
DB 11 TKDAKQ 17

```

Search completed: November 12, 2002, 11:48:26
 Job time : 28.25 secs

DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE Tomato golden mosaic virus subgenomic DNA derived from DNA B ccdds -
 DE covalently closed circular double-stranded molecule.
 OS Tomato golden mosaic virus (TGMV).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 NC NCB1_Taxid=10831;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87040767; PubMed=3022243;
 RA MacDowell S.W., Coutts R.H.A., Buck K.W.;
 RT "Molecular characterization of subgenomic single-stranded and double-
 RT stranded DNA forms isolated from plants infected with tomato golden
 RT mosaic virus".
 RL Nucleic Acids Res. 14:7967-7984(1986).
 DR EMBL; X04485; CAA28171.1; -
 DR InterPro: IPR000211; Gemin1.BL.
 DR Pfam: PF00845; Gemin1.BL; 1.
 SQ SEQUENCE 55 AA; 6281 MW; 41963570D739EC96 CRC64;

Query Match 1.6%; Score 7; DB 12; Length 55;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 312 SAKLSRS 318
 DB 43 SAKLSRS 49

RESULT 10
 ID 092FV7 PRELIMINARY; PRT; 68 AA.
 AC 092FV7:
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE Hypothetical protein RC1370.
 GN RC1370.
 OS Rickettsia conorii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiidae; Rickettsia.
 OX NCB1_Taxid=781;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MALISH 7;
 RX MEDLINE=21442074; PubMed=11557893;
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
 RA Raoult D.;
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";
 RL Science 293:2093-2098(2001).
 DR EMBL; AE008682; AAL03908.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 68 AA; 7373 MW; 98F44F56AE48EC6 CRC64;

Query Match 1.6%; Score 7; DB 16; Length 68;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 TALENKT 84
 DB 45 TALENKT 51

RESULT 11
 ID 091ZS4 PRELIMINARY; PRT; 72 AA.
 AC 091ZS4:
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
 DE Coat protein (Fragment).

GN CP.
 OS Potato virus Y strain NTN (PVY(NTN)).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Polyvirus.
 OX NCB1_Taxid=122280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUBER NECROSING;
 RA Cerovsky N., Piliyarova M., Moravec T., Petrzik K.;
 RT "Differences in nucleotide and amino acid sequences of N-terminal
 RT parts of coat proteins among isolates of potato virus Y-NTN strain";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF228634; AAF67875.1; -
 DR InterPro: IPR001592; Poty_coat.
 DR Pfam: PF00767; Poty_coat; 1.
 FT NON_TER 1
 FT NON_TER 72
 SQ SEQUENCE 72 AA; 7692 MW; 4F129B870523B482 CRC64;

Query Match 1.6%; Score 7; DB 12; Length 72;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 156 TKKDAKQ 162
 DB 11 TKKDAKQ 17

RESULT 12
 ID 091ZS5 PRELIMINARY; PRT; 72 AA.
 AC 091ZS5:
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
 DE Coat protein (Fragment).
 GN CP.
 OS Potato virus Y strain NTN (PVY(NTN)).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Polyvirus.
 OX NCB1_Taxid=122280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUBER NECROSING;
 RA Cerovsky N., Piliyarova M., Moravec T., Petrzik K.;
 RT "Differences in nucleotide and amino acid sequences of N-terminal
 RT parts of coat proteins among isolates of potato virus Y-NTN strain";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF228633; AAF67874.1; -
 DR InterPro: IPR001592; Poty_coat.
 DR Pfam: PF00767; Poty_coat; 1.
 FT NON_TER 1
 FT NON_TER 72
 SQ SEQUENCE 72 AA; 7721 MW; 2C5287E15624CBDD CRC64;

Query Match 1.6%; Score 7; DB 12; Length 72;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 156 TKKDAKQ 162
 DB 11 TKKDAKQ 17

RESULT 13
 ID 091ZS3 PRELIMINARY; PRT; 95 AA.
 AC 091ZS3:
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
 DE Coat protein (Fragment).
 GN CP.

GN MK1681.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AV19 / DSM 6324 / JCM 9639;
RA MEDLINE=21927647; PubMed=11930014;
RX Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natarale D.A., Rogozin I.B., Tatunov R.L., Wolf Y.I., Stettler K.O.,
RA Mal'khin A.G., Koonin E.V., Kozhavkin S.A.;
RT "The complete genome of hyperthermophilic Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL: AE010457; AM02894.1; -.
KW Complete proteome.
SQ SEQUENCE 227 AA; 24975 MW; B80099EE2BA8912 CRC64;

Query Match 1.8%; Score 8; DB 17; Length 227;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 LVHGETPA 112
Db 106 LVHGETPA 113

RESULT 6
Q9M268 PRELIMINARY; PRT; 299 AA.

AC Q9M268;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE RAV-like protein.
GN F21F14.140.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Choiane N., Robert C., Brotier P., Wincker P., Catolico L.,
RA Attiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K.,
RA Mayer K.F.X., Queller F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL338642; CAB71504.1; -.
DR InterPro: IPR003340; TF_B3.
DR Pfam: PF02362; B3; 1.
SQ SEQUENCE 299 AA; 34270 MW; 2AB841F179DD174B CRC64;

Query Match 1.8%; Score 8; DB 10; Length 299;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 174 SLSEFLDR 181
Db 292 SLSEFLDR 299

RESULT 7
Q9C122 PRELIMINARY; PRT; 306 AA.
AC Q9C122;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein PM1426.
GN PM1426.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PM70;
RX MEDLINE=2145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida PM70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL: AE006179; AK03510.1; -.
DR HSSP: P00631; 10D6.
DR InterPro: IPR003187; PLA1.
DR Pfam: PF02253; PLA1; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 306 AA; 35580 MW; EAF3DE8C1C22B26E CRC64;

Query Match 1.8%; Score 8; DB 16; Length 306;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 314 KLSRSMNR 321
Db 184 KLSRSMNR 191

RESULT 8
Q94ZC0 PRELIMINARY; PRT; 415 AA.

AC Q94ZC0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 2 (Fragment).
GN NAD2.
OS Isoetes duriei.
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Lycopodiophyta; Isoetopsida; Isoetales; Isoetaceae; Isoetes.
OX NCBI_TaxID=56743;
RN [1]
RP SEQUENCE FROM N.A.
RA Knop V.;
RT "An extended molecular land plant phylogeny.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
DR EMBL: AJ409119; CAC50076.1; -.
DR InterPro: IPR001750; Oxidored_g1.
DR InterPro: IPR003880; Ppantne_attach.
DR Pfam: PF00361; oxidored_g1; 1.
DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 415 AA; 45082 MW; E0D3ACCT820F6309 CRC64;

Query Match 1.8%; Score 8; DB 8; Length 415;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LSTLTLSI 12
Db 341 LSTLTLSI 348

RESULT 9
Q67608 PRELIMINARY; PRT; 55 AA.
AC Q67608;
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

OY 279 PEIFLTQPV 287
 |||||
 DB 221 PEIFLTQPV 229

RESULT 2

O9JT21 PRELIMINARY: PRT: 409 AA.

AC O9JT21. 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative phospholipase.
 GN NMA2021.
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_Taxid=65699;

SEQUENCE FROM N.A.
 [1]

RC STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;
 RX MEDLINE-20222556; PubMed-10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jags K., Leather S., Moule S., Mungall K., Quail M.A., Rasthead M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrall B.G.;
 RA "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491."
 RT Nature 404:502-506(2000).
 DR EMBL: AL162757; CAB5240.1; -
 DR HSSP: P0631; 10D5.
 DR InterPro: IPR003187; PLA1.
 DR Pfam: PF02253; PLA1; 1.
 KW Complete proteome.
 SQ SEQUENCE 409 AA; 45862 MW; CD6585B064D01A41 CRC64;

Query Match 2.0%; Score 9; DB 16; Length 409;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 279 PEIFLTQPV 287
 |||||
 DB 248 PEIFLTQPV 256

RESULT 3

O9CL62 PRELIMINARY: PRT: 862 AA.

AC O9CL62; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Cvsy.
 GN Cvsy OR PM1380.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OX NCBI_Taxid=747;

SEQUENCE FROM N.A.
 [1]

RC STRAIN-PM70;
 RX MEDLINE-21145866; PubMed-11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida pm70."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 CC -1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
 CC EMBL: AE006176; AAK03464.1; -
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR004358; Bact_sens_pr_C.
 DR InterPro: IPR003660; HAMP.

DR InterPro: IPR003661; His_kinA.
 DR InterPro: IPR004359; His_kin_sig.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam: PF00672; HAMP; 1.
 DR Pfam: PF02518; HATPase_C; 1.
 DR Pfam: PF00072; response_reg; 1.
 DR Pfam: PF00512; signal; 1.
 DR PRINTS: PR00344; BCTRLSENSOR.
 DR PRODOM: PD000039; Response_reg; 1.
 DR SMART: SM00304; HAMP; 1.
 DR SMART: SM00387; HATPase_C; 1.
 DR SMART: SM00388; HisKA; 1.
 DR SMART: SM00448; REC; 1.
 KW Kinase; Phosphorylation; Sensory transduction; Transferase;
 KW Complete proteome.
 SQ SEQUENCE 862 AA; 97846 MW; AB681A43B63626C0 CRC64;

Query Match 2.0%; Score 9; DB 16; Length 862;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LSTLTSL 13
 |||||
 DB 293 LSTLTSL 301

RESULT 4

O9AX85 PRELIMINARY: PRT: 1432 AA.

AC O9AX85; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative ABC transporter protein.
 GN P0410E03.7.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriarioidae; Oryzaceae; Oryza.
 OX NCBI_Taxid=4530;

SEQUENCE FROM N.A.
 [1]
 RC STRAIN-CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone: P0410E03."
 RL Submitted (Aug-2000) to the EMBL/Genbank/DBD databases.
 DR EMBL: AP002844; BAB21276.1; -
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003439; ABC_transporter.
 DR Pfam: PF00005; ABC_tran; 2.
 DR PRODOM: PD000006; ABC_transporter; 1.
 DR SMART: SM00382; AAA; 2.
 KW ATP-binding.
 SQ SEQUENCE 1432 AA; 160234 MW; 04E8CF2CA08D993 CRC64;

Query Match 2.0%; Score 9; DB 10; Length 1432;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 170 FPLSLSF 178
 |||||
 DB 830 FPLSLSF 838

RESULT 5

O8TUS3 PRELIMINARY: PRT: 227 AA.

AC O8TUS3; 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Predicted phosphatase of the PIP family.

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:46 ; Search time 26.25 Seconds
(without alignments)
3469.441 Million cell updates/sec

Title: US-09-787-083-8
Perfect score: 442
Sequence: 1 MKVSLSTLSTLILPCFAILA.....YNHATSFGVGLMDMGL 442

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_protent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriophage: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	2.0	382	16	09K0U7
2	9	2.0	409	16	09U0T21
3	9	2.0	862	16	09CL62
4	9	2.0	1432	10	09AX85
5	8	1.8	227	17	08RUS3
6	8	1.8	299	10	09M268
7	8	1.8	306	16	09CL22
8	8	1.8	415	8	094ZC0
9	7	1.6	55	12	067608
10	7	1.6	68	16	092FEV7
11	7	1.6	72	12	091ZS4
12	7	1.6	72	12	091ZS5
13	7	1.6	95	12	091ZS3
14	7	1.6	96	12	091ZS8
15	7	1.6	101	12	091ZS6
16	7	1.6	112	16	092HS2

17	7	1.6	122	16	09RU16	09RU16 delinococcus
18	7	1.6	124	12	091ZS7	091ZS7 potato viru
19	7	1.6	131	6	09GMD4	09GMD4 machaca fusc
20	7	1.6	138	12	091Z07	091Z07 potato viru
21	7	1.6	142	16	08RAS3	08RAS3 thermoaer
22	7	1.6	147	5	036035	036035 hexamita in
23	7	1.6	158	16	0929C1	0929C1 chlamydia p
24	7	1.6	164	16	097JH4	097JH4 clostridium
25	7	1.6	169	16	091ZAT7	091ZAT7 streptomyce
26	7	1.6	183	16	08YMM0	08YMM0 arabidopsi
27	7	1.6	186	10	09LIX9	09LIX9 arabidopsi
28	7	1.6	189	13	09DPT2	09DPT2 notolthenia
29	7	1.6	198	4	09BUX9	09BUX9 homo sapien
30	7	1.6	200	5	08T2L3	08T2L3 dictyostell
31	7	1.6	212	13	090ZNS5	090ZNS5 heteropneu
32	7	1.6	216	5	09VTR5	09VTR5 drosophi
33	7	1.6	216	2	09X6I6	09X6I6 streptococ
34	7	1.6	218	2	09RF14	09RF14 streptococ
35	7	1.6	219	5	017594	017594 caenorhabdl
36	7	1.6	220	2	09XCK1	09XCK1 streptococ
37	7	1.6	220	2	036036	036036 spironucle
38	7	1.6	221	12	065002	065002 alfalfa mos
39	7	1.6	227	5	09BMF4	09BMF4 glossina mo
40	7	1.6	233	6	09WZB0	09WZB0 ovis aries
41	7	1.6	233	16	08YH08	08YH08 brucella me
42	7	1.6	236	13	09DPS8	09DPS8 notolthenia
43	7	1.6	264	12	085260	085260 potato viru
44	7	1.6	265	9	038155	038155 bacterioph
45	7	1.6	266	12	091N40	091N40 potato viru

ALIGNMENTS

RESULT 1

ID	09K0U7	PRELIMINARY;	PRT;	382 AA.
AC	09K0U7			
DT	01-OCR-2000 (TREMURel. 15, Created)			
DT	01-OCR-2000 (TREMURel. 15, Last sequence update)			
DT	01-JUN-2002 (TREMURel. 21, Last annotation update)			
DE	Phospholipase A1, putative.			
GN	NMB0464.			
OS	Neisseria meningitidis (serogroup B).			
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=491;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MC58 / SEROGROUP B;			
RX	MEDLINE=20175755; PubMed=10710307;			
RA	Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,			
RA	Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,			
RA	Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,			
RA	Hait D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,			
RA	Mason T., Clecko A., Parksey D.S., Blair E., Ciltone H., Clark E.B.,			
RA	Cotton M.D., Uterback T.R., Khouri H., Qin H., Vamathevan J.,			
RA	Gill J., Scarlato V., Maignani V., Pizsa M., Grandi G., Sun L.,			
RA	Smith H.O., Fraser C.M., Moxon E.R., Rappunli R., Venter J.C.;			
RT	"Complete genome sequence of Neisseria meningitidis serogroup B strain			
RT	MC58."			
RL	Science 287:1809-1815(2000).			
DR	EMBL: AE002403; AAF40901.1;			
DR	HSSP: P00631; 10D5.			
DR	TIGR: NMB0464;			
DR	InterPro: IPR003187; PLAI.			
DR	Pfam: PF02253; PLAI; 1.			
KW	Complete proteome.			
SQ	SEQUENCE 382 AA; 42714 MW; B468A802F062E836 CRC64;			

Query Match 2.08; Score 9; DB 16; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RC SPECIES-MOUSE; PubMed=3785200;
 RA MEDLINE=87064538; Wang D., Dobner P., Dolph R., Lewis S.A., Cowan N.J.;
 RA Villaseca A., Wang D., Dobner P., Dolph R., Lewis S.A., Cowan N.J.;
 RT "Six mouse alpha-tubulin mRNAs encode five distinct isoforms: testis-
 RT specific expression of two sister genes";
 RL Mol. Cell. Biol. 6:2409-2419(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES-MOUSE; STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Itawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kodota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pease G., Quackenbush J.,
 RA Schirral L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Futuno M., Aono H., Baldarelli R., Barish G.,
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guenichet S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
 RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuk S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES-MOUSE;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
 CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
 CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
 CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
 CC -1- MISCELLANEOUS: THIS TUBULIN DOES NOT HAVE A C-TERMINAL TYROSINE.
 CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: X06956; CAA30026.1; -;
 DR EMBL: X04757; CAA28453.1; -;
 DR EMBL: BC009238; AAH09238.1; -;
 DR EMBL: M13444; AAA40502.1; -;
 DR EMBL: AK002427; BAB22094.1; -;
 DR EMBL: BC019959; AAH19959.1; -;
 DR PIR: A23873; A23873.
 DR KGD: AGI:1095410; Tuba4.
 DR InterPro: IPR000217; Tuba4.
 DR InterPro: IPR003008; Tubulin_Ftsz.
 DR Pfam: PF00091; tubulin; 1.
 DR PRINTS: PR01161; TUBULIN.
 DR PROSITE: PS00227; TUBULIN; 1.
 KW Microtubules; GTP-binding; Multigene family.
 FT NP_BIND 142 148 GTP (POTENTIAL).
 SQ SEQUENCE 448 AA; 49924 MW; CQ0ED90A183FE8F2 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 448;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 IKTKRSI 120
 |||||||

DB 335 IKTKRSI 341
 RESULT 15
 ID TBA5_CHICK STANDARD; PRT; 448 AA.
 AC P09644;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Tubulin alpha-5 chain.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_Taxid=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88296435; PubMed=3267229;
 RA Pratt L.F., Cleveland D.W.;
 RT "A survey of the alpha-tubulin gene family in chicken: unexpected
 RT sequence heterogeneity in the polypeptides encoded by five expressed
 RL genes";
 RL Embo J. 7:931-940(1988).
 CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
 CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
 CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
 CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
 CC -1- MISCELLANEOUS: THIS TUBULIN DOES NOT HAVE A C-TERMINAL TYROSINE.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST SEVEN ALPHA TUBULIN GENES
 CC (ALPHA-1 TO ALPHA-6, AND ALPHA-8), AND A PSEUDOGENE (ALPHA-7) IN
 CC CHICKEN.
 CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: X08061; CAA30852.1; ALT_INIT.
 DR PIR: S00470; UBCHAS.
 DR InterPro: IPR000217; Tubulin.
 DR InterPro: IPR003008; Tubulin_Ftsz.
 DR Pfam: PF00091; tubulin; 1.
 DR PRINTS: PR01161; TUBULIN.
 DR PROSITE: PS00227; TUBULIN; 1.
 KW Microtubules; GTP-binding; Multigene family.
 FT NP_BIND 142 148 GTP (POTENTIAL).
 SQ SEQUENCE 448 AA; 49948 MW; 2E498A2B20DCBA6 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 448;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 IKTKRSI 120
 |||||||
 DB 335 IKTKRSI 341

Search completed: November 12, 2002, 11:45:32
 Job time : 9.5 secs

DT 30-MAY-2000 (Rel. 39, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Probable ammonium transporter.
 GN AMT OR AMTB OR AQ_112.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
 OC Aquifex.
 RN NCBL_Taxid=63363;
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RA MEDLINE=98196666; PubMed=9537320;
 RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus."
 RL Nature 392:353-358(1998).
 CC -1- FUNCTION: INVOLVED IN THE UPTAKE OF AMMONIA (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE AMT/MEP/NRGA FAMILY OF AMMONIUM
 TRANSPORTERS (TC 2.49).

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 DR EMBL: AE000674; AAC06478.1;
 DR InterPro: IPR001905; Ammonium transp.
 DR Pfam: PF00909; Ammonium_transp; 1.
 DR TIGRfam: TIGR00836; amt; 1.
 DR PROSITE: PS01219; AMMONIUM_TRANSP; 1.
 KW Transport; Transmembrane; Complete proteome.
 FT TRANSMEM 3 23 POTENTIAL.
 FT TRANSMEM 31 51 POTENTIAL.
 FT TRANSMEM 64 84 POTENTIAL.
 FT TRANSMEM 123 143 POTENTIAL.
 FT TRANSMEM 150 170 POTENTIAL.
 FT TRANSMEM 183 203 POTENTIAL.
 FT TRANSMEM 217 237 POTENTIAL.
 FT TRANSMEM 246 266 POTENTIAL.
 FT TRANSMEM 278 298 POTENTIAL.
 FT TRANSMEM 301 321 POTENTIAL.
 FT TRANSMEM 331 351 POTENTIAL.
 FT TRANSMEM 374 394 POTENTIAL.
 SQ SEQUENCE 423 AA; 44322 MW; 166203BBB2A8A15B CRC64;

 Query Match 1.6%; Score 7; DB 1; Length 423;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 402 LGKGISG 408
 Db 104 LGKGISG 110

RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=93208376; PubMed=1296820;
 RA Coe I.R., Munro R., Sherwood N.M.;
 RT "Isolation of different brain-specific isoforms of alpha-tubulins
 RT from chum salmon (Oncorhynchus keta)."
 RL DNA Seq. 3:257-262(1992).
 CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
 CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
 CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
 CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
 CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.

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 DR EMBL: X66973; CAA47384.1;
 DR PIR: S25004; S25004.
 DR InterPro: IPR000217; Tubulin.
 DR InterPro: IPR003008; Tubulin_Fts2.
 DR Pfam: PF00091; tubulin; 1.
 DR PRINTS: PR01161; TUBULIN.
 DR PROSITE: PS00227; TUBULIN; 1.
 KW Microtubules; GTP-binding; Multigene family.
 DR NE_BIND 136 142 GTP (POTENTIAL).
 FT SITE 444 444 INVOLVED IN POLYMERIZATION.
 SQ SEQUENCE 444 AA; 49314 MW; C2CD75432DD6BAF CRC64;

 Query Match 1.6%; Score 7; DB 1; Length 444;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 114 IKTKRSI 120
 Db 329 IKTKRSI 335

RESULT 13
 TBA_ONCKE
 ID TBA_ONCKE STANDARD; PRT; 444 AA.
 AC P30436;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, last sequence update)
 DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE Tubulin alpha chain.
 OS Oncorhynchus keta (Chum salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 RN NCBL_Taxid=8018;
 RP SEQUENCE FROM N.A.

RESULT 14
 TBA4_HUMAN
 ID TBA4_HUMAN STANDARD; PRT; 448 AA.
 AC P05215;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Tubulin alpha-4 chain (Alpha-tubulin 4).
 GN TUBA4.
 OS Homo sapiens (Human).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN NCBL_Taxid=9606, 9541, 10090;
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human, and M. fascicularis;
 RX MEDLINE=87146332; PubMed=3029670;
 RA Dobner F.R., Kisilevskis E., Wentworth B.M., Villa-Komaroff L.;
 RT "Alternative 5' exons either provide or deny an initiator methionine
 RT codon to the same alpha-tubulin coding region."
 RL Nucleic Acids Res. 15:199-218(1987).
 RN NCBL_Taxid=9606, 9541, 10090;
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

CC INHIBITOR COMPLEX IN A MOLAR RATIO OF 1:1. IT IS HEAT RESISTANT AT
CC NEUTRAL AND ACIDIC PHs.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: MAY UNDERGO ACTIVATION AFTER SECRETION. IT IS PRODUCED
CC EXTRACELLULARLY IN MULTIPLE FORMS HAVING AT LEAST THREE DIFFERENT
CC MOLECULAR WEIGHTS (BBRP1-A, -B, AND -C).
CC -----
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CC -----
DR EMBL: D10696; BAA01538.1; -
KW Serine protease inhibitor; Protease inhibitor; Signal; Repeat.
FT SIGNAL 1 24
FT CHAIN 25 326 SERINE PROTEASE INHIBITOR.
FT CHAIN 104 326 SERINE PROTEASE INHIBITOR-C.
FT CHAIN 104 326 SERINE PROTEASE INHIBITOR-B (POTENTIAL).
FT CHAIN 122 326 SERINE PROTEASE INHIBITOR-A.
FT DOMAIN 177 304 CONTAINS TWO APPROXIMATE REPEATS.
FT REPEAT 177 208 1.
FT REPEAT 272 304 2.
SQ SEQUENCE 326 AA; 35100 MW; 1C0456ABFA912F77 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 326;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 PVAEVD 36
| | | | | | | |
Db 119 PVAEVD 125

RESULT 10
FLAD_METUA STANDARD; PRT; 342 AA.
AC 058305;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative flagella-related protein D.
GN FLAD OR Mj0895.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; Pubmed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RT Science 273:1058-1073(1996).
RL
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CC -----
CC -1- SIMILARITY: STRONG; TO M.VOLTAE FLAD, ALSO TO FLAE.
CC -----
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CC -----

CC EMBL: U67533; AAB98898.1; -
DR TIGR; Mj0895; -
KW Flagella; Complete proteome.
SQ SEQUENCE 342 AA; 39950 MW; B384DDDE1775566C CRC64;

Query Match 1.6%; Score 7; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PDLDY 362
| | | | | | | |
Db 255 PDLDY 261

RESULT 11
Y755_METUA STANDARD; PRT; 342 AA.
ID Y755_METUA
AC 058165;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein Mj0755 precursor.
DE Mj0755.
GN Methanococcus jannaschii.
OS Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; Pubmed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RT Science 273:1058-1073(1996).
RL
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CC -----
CC EMBL: U67521; AAB98748.1; -
DR TIGR; Mj0755; -
KW Hypothetical protein; Complete proteome.
FT SIGNAL 1 18
FT CHAIN 19 342 POTENTIAL.
FT CHAIN 19 342 HYPOTHETICAL PROTEIN Mj0755.
SQ SEQUENCE 342 AA; 38778 MW; BD25220A7EEND85C CRC64;

Query Match 1.6%; Score 7; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 YTTALEN 82
| | | | | | | |
Db 90 YTTALEN 96

RESULT 12
AMT_AQUAE STANDARD; PRT; 423 AA.
ID AMT_AQUAE
AC 065515;
DT 30-MAY-2000 (Rel. 39, Created)

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ID  LIVE.THEMA          STANDARD:          PRT:          273 AA.
AC  P74921:
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Probable branched-chain amino acid aminotransferase (EC 2.6.1.42)
DE  (BCAT).
GN  LIVE OR TM0831.
OS  Thermotoga maritima.
OC  Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
OC  Thermotogaceae; Thermotoga.
OX  NCBI_TaxID=2336;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=MSB8 / DSM 3109;
RX  MEDLINE=99287316; PubMed=10360571;
RA  Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
RA  Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA  McDonald L., Otterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA  Stewart A.M., Cottrell M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA  Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA  Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT  Evidence for lateral gene transfer between Archaea and Bacteria from
RT  genome sequence of Thermotoga maritima.
RL  Nature 399:323-329 (1999).
RN  [2]
RP  SEQUENCE OF 68-273 FROM N.A.
RC  STRAIN=MSB8 / DSM 3109;
RX  MEDLINE=97017137; PubMed=8863738;
RA  Guipaud O., Labedan B., Forterre P.;
RT  "A gyrB-like gene from the hyperthermophilic bacterium Thermotoga
RT  maritima".
RL  Gene 174:121-128 (1996).
CC  -1- FUNCTION: Acts on leucine, isoleucine and valine (By similarity).
CC  -1- CATALYTIC ACTIVITY: L-leucine + 2-oxoglutarate = 4-methyl-2-
CC  oxopentanoate + L-glutamate.
CC  -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC  -1- PATHWAY: Valine and isoleucine biosynthesis.
CC  -1- SIMILARITY: BELONGS TO CLASS-IV OF PYRIDOXAL- PHOSPHATE-DEPENDENT
CC  AMINOTRANSFERASES.
CC  -----
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CC  entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC  or send an email to license@sdb-sdb.ch).
CC  -----
DR  EMBL; AE001750; AAD35913.1; .
DR  EMBL; U49692; AAC4497.1; .
DR  HSSP; P00510; IASG.
DR  TIGR; TM0831; .
DR  InterPro: IPR001544; AminoTran_4.
DR  Pfam; PF01063; aminoTran_4; 1.
DR  ProDom; PD001961; AminoTran_4; 1.
DR  PROSITE; PS00770; AA_TRANSFER_CLASS_4; 1.
KW  Transferase; Amino transferase; Branched-chain amino acid biosynthesis;
KW  Pyridoxal phosphate; Complete; proteome.
FT  CONFLICT 77 AA: 31158 MW; 2162B705612E90E3 CRC64;
SQ  SEQUENCE 273 AA: 31158 MW; 2162B705612E90E3 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 273;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ID  M1A_PSEPU          STANDARD:          PRT:          322 AA.
AC  O30762:
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (IPP
DE  transferase) (isopentenyl-diphosphate:tRNA isopentenyltransferase)
DE  (IPPTase) (IPPT).
GN  M1A.
OS  Pseudomonas putida.
OC  Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC  Pseudomonas.
OX  NCBI_TaxID=303;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=M;
RA  Olekhnovich I.N., Gussis G.N.;
RT  Attenuation of the Pseudomonas putida trpE and trpGDC genes.
RL  Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: CATALYZES THE FIRST STEP IN THE BIOSYNTHESIS OF
CC  2-METHYLTIRIO-N6-(DELTA(2)-ISOPENTENYL)-ADENOSINE (MS121)[6A])
CC  ADJACENT TO THE ANTICODON OF SEVERAL tRNA SPECIES (BY SIMILARITY).
CC  -1- CATALYTIC ACTIVITY: isopentenyl diphosphate + tRNA = diphosphate +
CC  tRNA containing 6-isopentenyladenosine.
CC  -1- SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC  or send an email to license@sdb-sdb.ch).
CC  -----
DR  EMBL; AF016312; AAB69443.1; .
DR  InterPro: IPR002627; IPPT.
DR  Pfam; PF01715; IPPT; 1.
DR  ProDom; PD004674; IPPT; 1.
DR  TIGRFAMs; TIGR00174; m1a; 1.
KW  Transferase; Nucleotidyltransferase; tRNA processing; ATP-binding.
FT  NP_BIND 12 19
FT  SEQUENCE 322 AA: 35488 MW; D1AA81A2D7B32F6A CRC64;

Query Match 1.6%; Score 7; DB 1; Length 322;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ID  SPI_BACBR          STANDARD:          PRT:          326 AA.
AC  P43131:
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  01-NOV-1997 (Rel. 35, Last annotation update)
DE  Protease inhibitor precursor (BBRP1).
DE  Bacillus brevis.
OS  Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
OC  Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
OX  NCBI_TaxID=1393;
RN  [1]
RP  SEQUENCE FROM N.A., AND SEQUENCE OF 25-32; 104-112 AND 122-136.
RC  STRAIN=HPD31;
RX  MEDLINE=92304060; PubMed=1610177;
RA  Shiga Y., Hasegawa K., Tsuboi A., Yamagata H., Ueda S.;
RT  "Characterization of an extracellular protease inhibitor of Bacillus
RT  brevis HPD31 and nucleotide sequence of the corresponding gene.";
RL  Appl. Environ. Microbiol. 58:525-531 (1992).
CC  -1- FUNCTION: SHOWS INHIBITORY ACTIVITY TOWARDS SERINE PROTEASES, SUCH
CC  AS TRYPSIN, CHYMOTRYPSIN, AND SUBTILISIN. MAY FORM A TRYPSIN-

```

RL Mol. Mar. Biol. Biotechnol. 1:239-249(1992).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: PITUITARY GLANDS.
 CC -1- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
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 CC
 CC EMBL: AF267990; AAF82287.1; -
 DR HSP; Q28632; 1AN3.
 DR InterPro: IPR001400; Somatotropin.
 DR Pfam: PF00103; hormone; 2.
 DR PRINTS: PR00836; SOMATOTROPIN.
 DR PROSITE: PS00266; SOMATOTROPIN_1; 1.
 DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
 KW Hormone; Pituitary; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 212
 FT DISULFID 71 185 BY SIMILARITY.
 FT DISULFID 202 212 BY SIMILARITY.
 FT CONFLICT 91 91 G -> S (IN REF. 2).
 FT CONFLICT 128 128 T -> S (IN REF. 2).
 FT CONFLICT 203 203 D -> R (IN REF. 2).
 FT CONFLICT 203 203 D -> R (IN REF. 2).
 SQ SEQUENCE 212 AA; 23365 MW; 073FB7EB1DA573BE CRC64;
 Query Match 1.6%; Score 7; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 41 NDLAGDN 47
 Db 166 NDLAGDN 172
 RESULT 5
 ID TBA.OCTVU STANDARD; PRT; 240 AA.
 AC P24635;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Tubulin alpha chain (Fragment).
 OS Octopus vulgaris (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidae; Octopoda;
 OC Invertebrata; Octopodidae; Octopus.
 NC NCBI_TaxID=6645;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lens;
 RA Zinov'Eva R.D., Aleinikova K.S., Tomarev S.I.;
 RT "Isolation and structural characterization of cDNAs coding for alpha-
 RT tubulin of the octopus eye lens."
 RT Dokl. Akad. Nauk SSSR 302:462-467(1988).
 RL -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
 CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
 CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
 CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
 CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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 CC
 CC EMBL: X15845; CAA33844.1; -

DR PTR; A61544; A61544.
 DR InterPro: IPR000217; Tubulin.
 DR InterPro: IPR003008; Tubulin_Fts2.
 DR Pfam: PF00091; tubulin; 1.
 DR PROSITE: PS00227; TUBULIN; PARTIAL.
 KW Microtubules; GTP-binding.
 FT NON TER 1
 FT SITE 240 240
 SQ SEQUENCE 240 AA; 26961 MW; 13BB3A1E740FE2416 CRC64;
 Query Match 1.6%; Score 7; DB 1; Length 240;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 114 IKTRRSI 120
 Db 124 IKTRRSI 130
 RESULT 6
 ID Y304.MYCPN STANDARD; PRT; 270 AA.
 AC P75355;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical ABC transporter ATP-binding protein MG304 homolog
 DE (A05_or1270L).
 GN MPN433 OR MP408.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 NC NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; Pubmed=8948633;
 RA Himmelfreid R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
 RA Hermann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae."
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
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 CC
 CC EMBL: AE000040; AAB96056.1; -
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003439; ABC_transportr.
 DR Pfam: PF00005; ABC_tran; 1.
 DR Prodom: PD000006; ABC_transportr; 1.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW Hypothetical protein; ATP-binding; Transport; Complete proteome.
 KW NP_BIND
 FT NP_BIND 36
 SQ SEQUENCE 270 AA; 30770 MW; 6512640E4BC051B4 CRC64;
 Query Match 1.6%; Score 7; DB 1; Length 270;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 168 KQFPLS 174
 Db 125 KQFPLS 131
 RESULT 7
 ID IIVE_THDMA

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 431 GVGGLMND 438
 |||||
 DB 277 GVGGLMND 284

RESULT 2
 VITE_BPT5 STANDARD; PRT: 1396 AA.
 AC P13390; Q48502; 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 DE L-shaped tail fiber protein (LTF protein).
 GN LTF.
 OS Bacteriophage T5.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC T5-like viruses.
 OX NCBI_TaxID=10726;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95309401; PubMed=7789514;
 RA Kallman A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.,
 RA Kiyukov V.M.;
 RT "The nucleotide sequence of the bacteriophage T5 ltf gene.";
 RL FEBS Lett. 366:46-48(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kallman A.V.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]

PRELIMINARY PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE=88289370; PubMed=3267228;
 RA Kallman A.V., Kiyukov V.M., Bayev A.A.;
 RT "The nucleotide sequence of bacteriophage T5 DNA at the region
 between early and late genes.";
 RL Nucleic Acids Res. 16:6230-6230(1988).
 CC -1- FUNCTION: NONESSENTIAL PROTEIN THAT MEDIATES BINDING TO THE
 POLYMANNOSE O ANTIGEN.

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CC EMBL; X69460; CAA49220.1; -
 DR EMBL; AJ001191; CAA04591.1; -
 DR PIR; S01982; S01982.

KW Late protein.
 FT CONFLICT 986 V -> A (IN REF. 2).
 SQ SEQUENCE 1396 AA; 147989 MW; 18CD2192F65FFC1 CRC64;

Query Match 1.8%; Score 8; DB 1; Length 1396;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QSATQNAS 61
 |||||
 DB 87 QSATQNAS 94

RESULT 3
 TBA_PLAYO STANDARD; PRT: 197 AA.
 AC P12543;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Shulin alpha chain (Fragment).
 GN Shulin alpha chain (Fragment).
 OS Shulin alpha chain (Fragment).
 OC Shulin alpha chain (Fragment).
 OX Shulin alpha chain (Fragment).
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93364578; PubMed=1308206;
 RA Watanabe K., Igarashi A., Noso T., Chen T.T., Dunham R.A.,
 RA Kawachi H.;
 RT "Chemical identification of catfish growth hormone and prolactin.";

OS Plasmodium berghei yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5862;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=89014607; PubMed=2459618;
 RA Akella R., Arasu P., Valdivia A.B.;
 RT "Molecular clones of alpha-tubulin genes of Plasmodium yoelii reveal
 an unusual feature of the carboxy terminus.";
 RL Mol. Biochem. Parasitol. 30:165-174(1988).
 CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
 CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
 CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
 CC -1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
 CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.

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CC EMBL; M29816; AAA29779.1; -
 DR PIR; A54506; A54506.
 DR InterPro; IPR000217; Tubulin.
 DR InterPro; IPR003008; Tubulin_FtsZ.
 DR Pfam; PF00091; Tubulin; 1.
 DR PROSITE; PS00227; TUBULIN; PARTIAL.
 KW Microtubules; GTP-binding.
 FT NON TER 1

SQ SEQUENCE 197 AA; 2211 MW; 4DAAF199CC6CD319 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 IKTKRST 120
 |||||
 DB 82 IKTKRST 88

RESULT 4
 PRL_ICTPU STANDARD; PRT: 212 AA.
 AC P51904; Q91819;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Prolactin precursor (PRL).
 GN PRL.

OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OX NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE= Pituitary;
 RA Tang Y.;
 RT "A study on the channel catfish (Ictalurus punctatus) growth hormone
 RT gene family: structures of growth hormone and prolactin genes and
 RT somatolactin cDNA, their evolutionary implications and expression in
 RT the pituitary gland.";
 RL Thesis (1993), University of Maryland, U.S.A.
 RN [2]

RP SEQUENCE OF 27-212 FROM N.A.
 RC TISSUE= Pituitary;
 RX MEDLINE=93364578; PubMed=1308206;
 RA Watanabe K., Igarashi A., Noso T., Chen T.T., Dunham R.A.,
 RA Kawachi H.;
 RT "Chemical identification of catfish growth hormone and prolactin.";

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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:45 ; Search time 7.5 seconds

(without alignments)
2444.338 Million cell updates/sec

Title:

US-09-787-083-8

Sequence:

1 MKVSLSTLSTLSPCAFLA.....YNHEATSFVGGLMLNDMNGL 442

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched:

112892 seqs, 41476328 residues

Word size:

0

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	1.8	286	1	P37446 Klebsiella
2	8	1.8	1396	1	P13390 bacteriophage
3	7	1.6	197	1	P12543 plasmid
4	7	1.6	212	1	P51904 ictalurus p
5	7	1.6	240	1	P24635 octopus vul
6	7	1.6	270	1	P75355 mycoplasma
7	7	1.6	273	1	P74921 thermotoga
8	7	1.6	322	1	P43131 bacillus br
9	7	1.6	326	1	P58305 methanococc
10	7	1.6	342	1	P58165 methanococc
11	7	1.6	423	1	P06515 aquifex aeo
12	7	1.6	444	1	P30215 oncorhynch
13	7	1.6	448	1	P03644 gallus gall
14	7	1.6	448	1	P06604 diosiphila
15	7	1.6	449	1	P11480 physarum po
16	7	1.6	449	1	P08537 xenopus lae
17	7	1.6	450	1	P50238 physarum po
18	7	1.6	450	1	P50719 haemophilus
19	7	1.6	451	1	P05209 notophthalm
20	7	1.6	451	1	P04105 physarum po
21	7	1.6	451	1	P08537 xenopus lae
22	7	1.6	451	1	P50238 physarum po
23	7	1.6	451	1	P50719 haemophilus
24	7	1.6	451	1	P05209 notophthalm
25	7	1.6	451	1	P04105 physarum po
26	7	1.6	451	1	P08537 xenopus lae
27	7	1.6	451	1	P50238 physarum po
28	7	1.6	451	1	P50719 haemophilus
29	7	1.6	451	1	P05209 notophthalm
30	7	1.6	451	1	P04105 physarum po
31	7	1.6	451	1	P08537 xenopus lae
32	7	1.6	451	1	P50238 physarum po
33	7	1.6	451	1	P50719 haemophilus

34	7	1.6	681	1	CA02_HUMAN	Q99424 homo sapien
35	7	1.6	768	1	YB2_HUMAN	Q9117 homo sapien
36	7	1.6	783	1	FB2_HUMAN	O15117 homo sapien
37	7	1.6	862	1	AXN1_HUMAN	O15169 homo sapien
38	7	1.6	947	1	LKTA_PASSP	P5123 bacteriophage
39	7	1.6	1026	1	VG37_BP74	P03744 bacteriophage
40	7	1.6	3061	1	POLG_PVYHU	Q02963 p genome po
41	6	1.4	33	1	BR2B_RANES	P40838 rana esculie
42	6	1.4	33	1	BR2B_RANES	P32413 rana esculie
43	6	1.4	50	1	YK05_CAREL	P34300 caenorhabdi
44	6	1.4	51	1	INS_ACOCA	P01324 acornys cal
45	6	1.4	51	1	INS_ALLMI	P12703 alligator m

ALIGNMENTS

RESULT 1	ID	PAI_KLEPN	STANDARD	PRT	286 AA
AC	P37446				
DT	01-OCT-1994 (Rel. 30, Last sequence update)				
DT	01-OCT-1994 (Rel. 35, Last annotation update)				
DE	Phospholipase A1 precursor (EC 3.1.1.32) (Detergent-resistant phospholipase A) (DR-phospholipase A) (Phosphatidylcholine 1-acylhydrolase) (Outer membrane phospholipase A) (OM PLA).				
DE	Phospholipase A1 precursor (EC 3.1.1.32) (Detergent-resistant phospholipase A) (DR-phospholipase A) (Phosphatidylcholine 1-acylhydrolase) (Outer membrane phospholipase A) (OM PLA).				
GN	PLA.				
OS	Klebsiella pneumoniae.				
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;				
OX	Klebsiella.				
NCBI_TaxID=573;					
NP	SEQUENCE FROM N.A.				
RA	Medline-94131966; PubMed-8300539;				
RA	Brook R.G., P.M., Brinkman E., van Boxtel R., Bekkers A.C.A.P., Verheij H.M., Tomassen J.;				
RT	"Molecular characterization of enterobacterial plid genes encoding outer membrane phospholipase A."				
RL	J. Bacteriol. 176:861-870(1994).				
CC	-1- FUNCTION: HYDROLISIS OF PHOSPHATIDYLCHOLINE WITH PHOSPHOLIPASE A2 (EC 3.1.1.4) AND PHOSPHOLIPASE A1 (EC 3.1.1.32) ACTIVITIES.				
CC	-1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.				
CC	-1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 2-acylglycerophosphocholine + a fatty acid anion.				
CC	-1- COFACTOR: REQUIRES CALCIUM IONS FOR ACTIVITY.				
CC	-1- SUBCELLULAR LOCATION: OUTER MEMBRANE; ONE OF THE VERY FEW ENZYMES LOCATED THERE.				
CC	-----				
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CC	-----				
DR	EMBL; X76901; CA54223.1; -				
DR	PIR; B36971; B36971.				
DR	PIR; S40129; S40129.				
DR	HSSP; P00631; 10D6.				
DR	InterPro; IPR003187; PLA1.				
DR	Pfam; PF02253; PLA1.1				
DR	PRINTS; PR01486; PMPHLIPASEA1.				
KW	Hydrolase; Lipid degradation; Outer membrane; Signal; Calcium.				
FT	CHAIN 1 20				
FT	SIGNAL 1 20				
FT	CHAIN 21 286				
FT	ACT SITE 161 161				
SO	SEQUENCE 286 AA; 32544 MW; 3E39F63085108A3 CXC64;				
Query Match	1.8%; Score 8; DB 1; Length 286;				
Best Local Similarity	100.0%; Pred. No. 1.6;				

A:Residues: 1-183 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA076612.1; PID:g17134051; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr4913

Query Match 1.6%; Score 7; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 EVRSEND 42
 DB 104 EVRSEND 110

RESULT 13
 A54506
 tubulin alpha-1 chain - Plasmodium yoelii (fragment)
 C:Species: Plasmodium yoelii
 C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 13-Aug-1999
 C:Accession: A54506
 R:Arkella, R.; Arasu, P.; Valdiva, A.B.
 Mol. Biochem. Parasitol. 30, 163-174, 1988
 A>Title: Molecular clones of alpha-tubulin genes of Plasmodium yoelii reveal an unusual
 A:Reference number: A54506; MUID:89014607; PMID:2459618
 A:Accession: A54506
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-197 <AKE>
 A:Cross-references: GB:M29816; NID:g160729; PIDN:AAA29779.1; PID:g160730
 C:Superfamily: tubulin

Query Match 1.6%; Score 7; DB 2; Length 197;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 IKTKRSI 120
 DB 82 IKTKRSI 88

RESULT 14
 T19438
 hypothetical protein C25A1.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T19438
 R:Mortimore, B.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19124
 A:Accession: T19438
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-219 <WIL>
 A:Cross-references: EMBL:Z81038; PIDN:CAB02762.1; GSPDB:GN00019; CESP:C25A1.1
 A:Experimental source: clone C25A1
 C:Genetics:
 A:Gene: CESP:C25A1.1
 A:Map position: 1
 A:introns: 33/1; 66/1; 151/2

Query Match 1.6%; Score 7; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 KDAKOLE 164
 DB 52 KDAKOLE 58

RESULT 15
 AD3344
 hypothetical protein BMEI0738 [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis
 C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
 C:Accession: AD3344
 R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
 .; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A>Title: The genome sequence of the facultative intracellular pathogen Brucella melit
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AD3344
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <KUR>
 A:Cross-references: GB:AE008917; PIDN:AAL51919.1; PID:g17982674; GSPDB:GN00190
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI0738
 A:Map position: 1

Query Match 1.6%; Score 7; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 26 AVPNPVA 32
 DB 160 AVPNPVA 166

Search completed: November 12, 2002, 11:46:32
 Job time : 14.75 secs

C:Genetics:
A:Gene: RC0699

Query Match
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 NDGODN 47
|||||||
Db 85 NDGODN 91

RESULT 8

E75377
hypothetical protein - *Deinococcus radiodurans* (strain R1)

C:Species: *Deinococcus radiodurans*
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: E75377
R:White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Me
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: E75377
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-122 <WHIT>
A:Cross-references: GB:AE002002; GB:AE00513; NID:96459345; PIDN:AAF1150.1; PID:9645935
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRI580
A:Map position: 1

Query Match
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 EHEPELY 76
|||||||
Db 115 EHEPELY 121

RESULT 9

E86498
Pts IIA Protein [imported] - *Chlamydomonas reinhardtii* (strain J138)

C:Species: *Chlamydomonas reinhardtii*, *Chlamydomonas reinhardtii*
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: E86498
R:Shirai, M.; Hiraoka, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of *Chlamydomonas reinhardtii* J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: E86498
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <STRO>
A:Cross-references: GB:BA000008; NID:98978434; PIDN:BAA98271.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: ptnN_1
C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannitol-5

Query Match
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSTLTLS 11
|||||||
Db 126 LSTLTLS 132

RESULT 10

E72124

pts iia protein - *Chlamydomonas reinhardtii* (strain CML029)

C:Species: *Chlamydomonas reinhardtii*, *Chlamydomonas reinhardtii*
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C:Accession: E72124
R:Kaltan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of *Chlamydomonas reinhardtii* and *C. trachomatis*.
A:Reference number: A72000; MUID:99206606; PMID:10192388

A:Accession: E72124
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <ARN>
A:Cross-references: GB:AE001591; GB:AE001363; NID:94376311; PIDN:ABD18213.1; PID:9437
A:Experimental source: strain CML029
C:Genetics:
A:Gene: ptnN_1
C:Superfamily: phosphotransferase system enzyme II; phosphotransferase system mannitol-5

F:28-156/Domain: phosphotransferase system mannitol-specific enzyme II factor III hom

Query Match
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSTLTLS 11
|||||||
Db 126 LSTLTLS 132

RESULT 11

E97061
Integrase XerD family protein (similarity only with C-terminal part) [imported] - *Clo*

C:Species: *Clostridium acetobutylicum*
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: E97061
R:Noelling, M.J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L
J. Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A:Reference number: A96900; MUID:21353325; PMID:21353325
A:Accession: E97061
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-164 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK79280.1; PID:G15024240; GSPDB:GN00168
A:Experimental source: *Clostridium acetobutylicum* ATCC824
C:Genetics:
A:Gene: CAC1310

Query Match
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 QLENKSN 378
|||||||
Db 49 QLENKSN 55

RESULT 12

A12419
hypothetical protein alr4913 [imported] - *Nostoc* sp. (strain PCC 7120)

C:Species: *Nostoc* sp.
C>Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: A12419
R:Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriju
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: A12419
A:Status: preliminary
A:Molecule type: DNA

Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 PEFLTPQPV 287
|||||
DB 248 PEFLTPQPV 256

RESULT 3

B36971

outer membrane phospholipase A (EC 3.1.1.-) precursor - Klebsiella pneumoniae
C:Species: Klebsiella pneumoniae

C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 18-Jun-1999

C:Accession: B36971; S40129

R:Brok, R.G.P.M.; Brinkman, E.; van Bortel, R.; Bekkers, A.C.A.P.A.; Verheij, H.M.; Tomm

J. Bacteriol. 176, 861-870, 1994

A:Title: Molecular characterization of enterobacterial plid genes encoding outer membran

A:Reference number: A36971; MUID:94131966; PMID:8300539

A:Accession: B36971

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-286 <BRO>

A:Cross-references: EMBL:X76901; NID:9436880; PIDN:CAA54223.1; PID:9436881

A:Note: authors translated the codon AAG for residue 112 as Arg

C:Genetics:

A:Gene: plid

C:Superfamily: bacterial phospholipase A1

C:Keywords: carboxylic ester hydrolase

Query Match

Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 GVGMLND 438
|||||
DB 277 GVGMLND 284

RESULT 4

T47989

RAV-like protein - Arabidopsis thaliana

N:Alternate names: protein F21F14.140

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: T47989

R:Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Se

submitted to the Protein Sequence Database, February 2000

A:Reference number: Z24481

A:Accession: T47989

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-299 <CHO>

A:Cross-references: EMBL:AL138642

A:Experimental source: cultivar Columbia; BAC clone F21F14

A:Genetics:

A:Map position: 3

A:Note: F21F14.140

Query Match 1.8%; Score 8; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 SLSPDLDR 181
|||||
DB 292 SLSPDLDR 299

RESULT 5

S36851

L-shaped tail fiber protein - phage T5
N:Alternate names: ltf protein

C:Species: phage T5

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000

C:Accession: S65934; S01984; S36851

R:Kallman, A.V.; Kulshin, V.E.; Shlyapnikov, M.G.; Ksenzenko, V.N.; Kryukov, V.M.

FEBS Lett. 366, 46-48, 1995

A:Title: The nucleotide sequence of the bacteriophage T5 ltf gene.

A:Reference number: S65934; MUID:95309401; PMID:7789514

A:Accession: S65934

A:Molecule type: DNA

A:Residues: 1-1396 <KAL>

A:Cross-references: EMBL:X69460; NID:915415; PIDN:CAA49220.1; PID:915416

R:Kallman, A.V.; Kryukov, V.M.; Bayev, A.A.

Nucleic Acids Res. 16, 6230, 1988

A:Title: The nucleotide sequence of bacteriophage T5 DNA at the region between early

A:Reference number: S01984; MUID:88289370; PMID:3267228

A:Accession: S01984

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 934-985, 'A', 987-1396 <KA2>

A:Cross-references: EMBL:X07559

C:Genetics:

A:Gene: ltf

C:Keywords: late protein; tail fiber

Query Match 1.8%; Score 8; DB 2; Length 1396;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QSATOSAS 61
|||||
DB 87 QSATOSAS 94

RESULT 6

B97871

hypothetical protein RC1370 [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001

C:Accession: B97871

R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;

Science 293, 2093-2098, 2001

A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; MUID:21442074; PMID:11557893

A:Accession: B97871

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-68 <KUR>

A:Cross-references: GB:AE006914; PIDN:AAL03908.1; PID:915620515; GSPDB:GN00173

C:Genetics:

A:Gene: RC1370

Query Match 1.6%; Score 7; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 TALENKT 84
|||||
DB 45 TALENKT 51

RESULT 7

C97787

hypothetical protein RC0699 [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001

C:Accession: C97787

R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;

Science 293, 2093-2098, 2001

A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; MUID:21442074; PMID:11557893

A:Accession: C97787

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-112 <KUR>

A:Cross-references: GB:AE006914; PIDN:AAL03237.1; PID:915619790; GSPDB:GN00173

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:45 ; Search time 13.75 Seconds
(without alignments)
3090.285 Million cell updates/sec

Title: US-09-787-083-8

Perfect score: 442

Sequence: 1 MKVSLSTLNLILPCFALA.....YNHEATSPGVGLMLNDMGL 442

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	2.0	382	2	phospholipase A1,
2	9	2.0	409	2	probable phospholip
3	8	1.8	286	2	outer membrane pho
4	8	1.8	289	2	RAV-like protein -
5	8	1.8	1396	2	L-shaped tail fibe
6	7	1.6	68	2	hypothetical prote
7	7	1.6	112	2	hypothetical prote
8	7	1.6	122	2	hypothetical prote
9	7	1.6	158	2	hypothetical prote
10	7	1.6	158	2	pts IIA protein [1
11	7	1.6	164	2	pts IIA protein -
12	7	1.6	183	2	integrase xerD fam
13	7	1.6	197	2	hypothetical prote
14	7	1.6	219	2	tubulin alpha-1 ch
15	7	1.6	233	2	hypothetical prote
16	7	1.6	240	2	hypothetical prote
17	7	1.6	264	2	tubulin alpha chal
18	7	1.6	267	2	coat protein - pot
19	7	1.6	267	2	coat protein - pot
20	7	1.6	267	2	genome polyprotein
21	7	1.6	267	2	capsid protein - p
22	7	1.6	267	2	coat protein - p
23	7	1.6	270	2	tail fiber protein
24	7	1.6	273	2	abc transport ATP-
25	7	1.6	288	2	transaminase B hom
26	7	1.6	306	2	probable phosphotr
27	7	1.6	307	2	hypothetical prote
28	7	1.6	310	2	hydrolyase, probabl
29	7	1.6	313	2	polyprotein - pota

30	7	1.6	321	2	H82240	conserved hypotnet
31	7	1.6	324	2	T23876	hypothetical prote
32	7	1.6	326	2	A43939	proteinase inhibit
33	7	1.6	338	2	F69437	hypothetical prote
34	7	1.6	341	2	T47653	pectate lyase-like
35	7	1.6	342	2	G64411	hypothetical prote
36	7	1.6	343	2	C64394	hypothetical prote
37	7	1.6	349	2	AG2465	hypothetical prote
38	7	1.6	349	2	T43920	yfcu protein [impo
39	7	1.6	349	2	G90400	hypothetical prote
40	7	1.6	370	2	G83219	probable dihydrol
41	7	1.6	379	2	S13556	genome polyprotein
42	7	1.6	381	2	G82132	ribonuclease D VC1
43	7	1.6	382	2	S13337	tail fiber protein
44	7	1.6	384	2	S70638	tubulin alpha chal
45	7	1.6	384	2	S70641	tubulin alpha chal

ALIGNMENTS

RESULT 1
E81195
phospholipase A1, probable NMB0464 [imported] - Neisseria meningitidis (strain MC58 s
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: E81195
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiagani, V.; Plazzi, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.;
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MIMD:20175755; PMID:10710307
A:Accession: E81195
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-382 <RET>
A:Cross-references: GB:AE002403; GB:AE002098; NID:g7225688; PIDN:ANF40901.1; PID:g722
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0464

Query Match 2.0%; Score 9; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 PEFLRQPV 287
|||
Db 221 PEFLRQPV 229

RESULT 2
H81831
probable phospholipase NMA2021 [imported] - Neisseria meningitidis (strain Z2491 serog
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: H81831
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: AB1775; MIMD:20222556; PMID:10761919
A:Accession: H81831
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <PAR>
A:Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85240.1; PID:g738
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA2021

Query Match 2.0%; Score 9; DB 2; Length 409;

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; OTHER INFORMATION: MAP TO AL031587.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
US-09-864-761-43426

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Query Match      1.4% Score 6; DB 10; Length 26;
Best Local Similarity 100.0%; Pred.No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 345 KEGSGS 350
  |||||
Db 9 KEGSGS 14

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Search completed: November 12, 2002, 11:49:44
 Job time : 7.75 secs

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; PRIOR FILING DATE: 1992-11-16
; PRIOR APPLICATION NUMBER: 07/453,445
; PRIOR FILING DATE: 1989-12-20
; PRIOR APPLICATION NUMBER: 07/416,218
; PRIOR FILING DATE: 1989-10-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-844-1

Query Match
Best Local Similarity 100.0%; Score 6; DB 10; Length 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 LYOLEN 375
Db 13 LYOLEN 18

RESULT 13
US-09-815-229-1
; Sequence 1, Application US/09815229
; Patent No. US20020058614A1
; GENERAL INFORMATION:
; APPLICANT: Filvaroff, Ellen H.
; APPLICANT: Okumu, Franklin W.
; TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGINOUS DISORDERS
; FILE REFERENCE: P176R1US
; CURRENT APPLICATION NUMBER: US/09/815,229
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/192,103
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-815-229-1

Query Match
Best Local Similarity 100.0%; Score 6; DB 10; Length 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 LYOLEN 375
Db 13 LYOLEN 18

RESULT 14
US-10-066-151-102
; Sequence 102, Application US/10066151
; Patent No. US20020132300A1
; GENERAL INFORMATION:
; APPLICANT: Hogan, Patrick G.
; APPLICANT: Rao, Anjana
; APPLICANT: Aramburu, Jose
; TITLE OF INVENTION: SPECIFIC INHIBITORS OF NFAT ACTIVATION
; TITLE OF INVENTION: BY CALCIUM-INDUCED AND THEIR USE IN TREATING IMMUNE-RELATED
; FILE REFERENCE: 10861-004002
; CURRENT APPLICATION NUMBER: US/10/066,151
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 09/248,620
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/074,467
; PRIOR FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 22
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide containing the
; OTHER INFORMATION: SPIRITPS amino acid sequence
US-10-066-151-102

Query Match
Best Local Similarity 100.0%; Score 6; DB 12; Length 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 212 TPSHEA 217
Db 15 TPSHEA 20

RESULT 15
US-09-864-761-43426
; Sequence 43426, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecmcca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43426
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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OY 415 GYGSL 420
11 GYGSL 16

RESULT 10

US-09-947-563-1
; Sequence 1, Application US/09947563
; Patent No. US20020156234A1
; GENERAL INFORMATION:

APPLICANT: Rubroder, Franz-Josef

Keller, Reinhold

TITLE OF INVENTION: Improved process for obtaining

insulin precursors having correctly bonded cystine bridges

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Flinagan, Henderson, Farrabow, Garrett &

Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/947,563

FILING DATE: 07-Sep-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/134,836

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Leslie McDowell

REGISTRATION NUMBER: 34,872

REFERENCE/DOCKET NUMBER: 02481.1600-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Escherichia coli

FEATURE:

NAME/KEY: Protein

LOCATION: 1..21

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-947-563-1

Query Match 1.4%; Score 6; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 LYOLEN 375
13 LYOLEN 18

RESULT 11

US-09-947-563-7

; Sequence 7, Application US/09947563

; Patent No. US20020156234A1

; GENERAL INFORMATION:

APPLICANT: Rubroder, Franz-Josef

Keller, Reinhold
TITLE OF INVENTION: Improved process for obtaining
insulin precursors having correctly bonded cystine bridg

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Flinagan, Henderson, Farrabow, Garrett &

Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/947,563

FILING DATE: 07-Sep-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/134,836

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Leslie McDowell

REGISTRATION NUMBER: 34,872

REFERENCE/DOCKET NUMBER: 02481.1600-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Escherichia coli

FEATURE:

NAME/KEY: Protein

LOCATION: 1..21

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-947-563-7

Query Match 1.4%; Score 6; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 LYOLEN 375
13 LYOLEN 18

RESULT 12

US-09-853-844-1

; Sequence 1, Application US/09853844

; Patent No. US20020013269A1

; GENERAL INFORMATION:

APPLICANT: Balschmidt, Per

Brange, Vellgaard Jens Jorgen

TITLE OF INVENTION: Human Insulin Analogues

FILE REFERENCE: 3343.270-US

CURRENT APPLICATION NUMBER: US/09/853,844

PRIOR FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 08/965,221

PRIOR FILING DATE: 1997-11-06

PRIOR APPLICATION NUMBER: 08/531,842

PRIOR FILING DATE: 1995-09-21

PRIOR APPLICATION NUMBER: 08/275,196

PRIOR FILING DATE: 1994-07-14

PRIOR APPLICATION NUMBER: 07/976,805

APPLICANT: Frank B. Gertler
APPLICANT: Jorgen Wehland
TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
FILE REFERENCE: M0656/7065
CURRENT APPLICATION NUMBER: US/09/825,144
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/194,215
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 783
TYPE: PRT
ORGANISM: Homo sapiens
US-09-825-144-2

Query Match 1.6%; Score 7; DB 10; Length 783;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 268 NSRPFV 274
Db 17 NSRPFV 23

RESULT 7
US-09-825-144-4
Sequence 4, Application US/09825144
Patent No. US20020037286A1
GENERAL INFORMATION:
APPLICANT: Mathias Krause
APPLICANT: Antonio S. Sechl
APPLICANT: Frank B. Gertler
APPLICANT: Jorgen Wehland
TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
FILE REFERENCE: M0656/7065
CURRENT APPLICATION NUMBER: US/09/825,144
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/194,215
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 829
TYPE: PRT
ORGANISM: Homo sapiens
US-09-825-144-4

Query Match 1.6%; Score 7; DB 10; Length 829;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 268 NSRPFV 274
Db 17 NSRPFV 23

RESULT 8
US-09-947-770-20
Sequence 20, Application US/09947770
Patent No. US20020068715A1
GENERAL INFORMATION:
APPLICANT: Steinman, Lawrence
APPLICANT: Ruiz, Pedro
APPLICANT: Garten, Hideki
TITLE OF INVENTION: DNA Vaccination for Treatment of
FILE REFERENCE: STAN123CIP
CURRENT APPLICATION NUMBER: US/09/947,770
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: PCT/US00/06233
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 09/267,590

PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Insulin A (7-21) peptide
US-09-947-770-20

Query Match 1.4%; Score 6; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 LYOLEN 375
Db 7 LYOLEN 12

RESULT 9
US-09-732-561-23
Sequence 23, Application US/09732561
Patent No. US20020035738A1
GENERAL INFORMATION:
APPLICANT: Thoma, Bart
APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Kazan, Kemal
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA Ag Products
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-732-561-23

Query Match 1.4%; Score 6; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; TITLE OF INVENTION: GENES THAT REGULATE HEMATOPOIETIC BLOOD FORMING STEM
; FILE OF INVENTION: CELLS AND USES THEREOF
; FILE REFERENCE: 2275-1-005
; CURRENT APPLICATION NUMBER: US/09/789,919
; CURRENT FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-789-919-42
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Query Match          1.6%; Score 7; DB 10; Length 158;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 212 TFSHEAK 218
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DB 11 TFSHEAK 17
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```
RESULT 3
US-09-773-882-2
; Sequence 2, Application US/09773882
; Patent No. US20020106769A1
; GENERAL INFORMATION:
; APPLICANT: Omura, Mitsuo
; APPLICANT: Inagaki, Tomoko
; APPLICANT: Matsumoto, Ryoji
; APPLICANT: Moriguchi, Takaya
; APPLICANT: Hasegawa, Shin
; TITLE OF INVENTION: UDP-D-Glucose:Limonicid Glucosyltransferase
; FILE REFERENCE: 0119.98
; CURRENT APPLICATION NUMBER: US/09/773,882
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-021179
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Citrus unshiu
US-09-773-882-2
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```
Query Match          1.6%; Score 7; DB 10; Length 511;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 32 AFVDEVR 38
    |||||
DB 459 AFVDEVR 465
```

```
RESULT 4
US-09-773-882-11
; Sequence 11, Application US/09773882
; Patent No. US20020106769A1
; GENERAL INFORMATION:
; APPLICANT: Omura, Mitsuo
; APPLICANT: Inagaki, Tomoko
; APPLICANT: Matsumoto, Ryoji
; APPLICANT: Moriguchi, Takaya
; APPLICANT: Hasegawa, Shin
; APPLICANT: Suhayda, Charles
; TITLE OF INVENTION: UDP-D-Glucose:Limonicid Glucosyltransferase
; FILE REFERENCE: 0119.98
; CURRENT APPLICATION NUMBER: US/09/773,882
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-021179
; PRIOR FILING DATE: 2000-01-31
```

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; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Citrus unshiu
US-09-773-882-11
```

```
Query Match          1.6%; Score 7; DB 10; Length 511;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 32 AFVDEVR 38
    |||||
DB 459 AFVDEVR 465
```

```
RESULT 5
US-09-815-242-11029
; Sequence 11029, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11029
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-11029
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Query Match          1.6%; Score 7; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 168 KOFPLS 174
    |||||
DB 434 KOFPLS 440
```

```
RESULT 6
US-09-825-144-2
; Sequence 2, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Mathias Krause
; APPLICANT: Antonio S. Secchi
```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:45:00 ; Search time 5.75 Seconds

(without alignments)
1108.344 Million cell updates/sec

Title: US-09-787-083-8

Perfect score: 442
Sequence: 1 MKVSLSTLTSLTILPCFALLA.....YNHEATSGVGLMLNDWML 442Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 92612 seqs, 14418503 residues

Word size : 0

Total number of hits satisfying chosen parameters: 92612

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications, AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep: *
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep: *
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	1.6	75	10	US-09-764-869-1013 Sequence 1013, App
2	7	1.6	158	10	US-09-789-919-42 Sequence 42, App
3	7	1.6	511	10	US-09-773-882-2 Sequence 2, App1
4	7	1.6	511	10	US-09-773-882-11 Sequence 11, App1
5	7	1.6	513	10	US-09-815-242-11029 Sequence 9, App1
6	7	1.6	783	10	US-09-825-144-2 Sequence 2, App1
7	7	1.6	829	10	US-09-825-144-4 Sequence 4, App1
8	6	1.4	15	10	US-09-947-770-20 Sequence 20, App1
9	6	1.4	17	10	US-09-732-561-23 Sequence 23, App1
10	6	1.4	21	9	US-09-947-563-1 Sequence 1, App1
11	6	1.4	21	10	US-09-853-844-1 Sequence 1, App1
12	6	1.4	21	10	US-09-813-229-1 Sequence 1, App1
13	6	1.4	22	12	US-10-066-151-102 Sequence 102, App
14	6	1.4	26	10	US-09-864-761-43426 Sequence 43426, A
15	6	1.4	28	12	US-10-014-269-9 Sequence 9, App1
16	6	1.4	30	10	US-09-815-229-16 Sequence 16, App1
17	6	1.4	33	10	US-09-030-619-175 Sequence 175, App
18	6	1.4	39	10	US-09-205-658-116 Sequence 116, App
19	6	1.4	10	10	US-09-764-869-1013

20	6	1.4	39	12	US-10-042-417-18	Sequence 18, App1
21	6	1.4	46	10	US-09-205-658-132	Sequence 132, App
22	6	1.4	46	10	US-09-205-658-133	Sequence 133, App
23	6	1.4	46	10	US-09-205-658-136	Sequence 136, App
24	6	1.4	48	10	US-09-891-171-10	Sequence 10, App1
25	6	1.4	50	10	US-09-853-844-4	Sequence 4, App1
26	6	1.4	50	10	US-09-864-761-41965	Sequence 41965, A
27	6	1.4	51	9	US-10-028-410-3	Sequence 3, App1
28	6	1.4	54	10	US-09-815-229-13	Sequence 13, App1
29	6	1.4	56	10	US-09-864-761-41804	Sequence 41804, A
30	6	1.4	64	10	US-09-864-761-36407	Sequence 36407, A
31	6	1.4	73	12	US-10-062-254-16	Sequence 16, App1
32	6	1.4	77	10	US-09-864-761-42061	Sequence 42061, A
33	6	1.4	78	10	US-09-864-761-38666	Sequence 38666, A
34	6	1.4	81	10	US-09-799-514-14	Sequence 14, App1
35	6	1.4	86	9	US-09-878-380-1	Sequence 1, App1
36	6	1.4	86	9	US-10-028-410-2	Sequence 2, App1
37	6	1.4	90	10	US-09-887-586A-35	Sequence 35, App1
38	6	1.4	90	10	US-09-903-012-35	Sequence 35, App1
39	6	1.4	91	10	US-09-864-761-46089	Sequence 46089, A
40	6	1.4	91	10	US-09-815-242-5022	Sequence 5022, App
41	6	1.4	91	10	US-09-815-242-10688	Sequence 10688, A
42	6	1.4	96	9	US-09-947-563-4	Sequence 4, App1
43	6	1.4	96	9	US-09-947-563-5	Sequence 5, App1
44	6	1.4	96	12	US-10-062-254-18	Sequence 18, App1
45	6	1.4	99	10	US-09-764-869-1082	Sequence 1082, App

ALIGNMENTS

RESULT 1
US-09-764-869-1013
Sequence 1013, Application US/09764869
Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764, 869
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1013
LENGTH: 75
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (61)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (74)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-869-1013

Query Match 1.6%: Score 7; DB 10; Length 75;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VSLSTLT 9
|||||
Db 44 VSLSTLT 50

RESULT 2
US-09-789-919-42
Sequence 42, Application US/09789919
Patent No. US20020064855A1
GENERAL INFORMATION:
APPLICANT: Lemischka, Thor
APPLICANT: Moore, Katerl

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; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14
; OTHER INFORMATION: /product- "Ser or Tyr"
US-08-974-775-32
    
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Query Match          1.4%; Score 6; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    
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OY 424 NHEATS 429
   |||||
Db 8 NHEATS 13
    
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Search completed: November 12, 2002, 11:49:15
 Job time : 12 secs

RESULT 13
US-08-974-775-9
; Sequence 9, Application US/08974775
; Patent No. 6096706
; GENERAL INFORMATION:
; APPLICANT: Toback, F. Gary
; APPLICANT: Walsh-Reitz, Margaret
; TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
; TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
; STREET: NBC Tower - Suite 3600, 455 N. Cityfront
; STREET: Plaza Drive
; CITY: Chicago
; STATE: Illinois
; ZIP: 60611-5599
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,775
; FILING DATE: 20-NOV-1997
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin, Alice O.
; REGISTRATION NUMBER: 35,601
; REFERENCE/DOCKET NUMBER: 7814/27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-321-4200
; TELEFAX: 312-321-4299
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-775-9
Query Match 1.4%; Score 6; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 424 NHEATS 429
DB 8 NHEATS 13

RESULT 15
US-08-974-775-10
; Sequence 32, Application US/08974775
; Patent No. 6096706
; GENERAL INFORMATION:
; APPLICANT: Toback, F. Gary
; APPLICANT: Walsh-Reitz, Margaret
; TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
; TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
; STREET: NBC Tower - Suite 3600, 455 N. Cityfront
; STREET: Plaza Drive
; CITY: Chicago
; STATE: Illinois
; ZIP: 60611-5599
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,775
; FILING DATE: 20-NOV-1997
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin, Alice O.
; REGISTRATION NUMBER: 35,601
; REFERENCE/DOCKET NUMBER: 7814/27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-321-4200
; TELEFAX: 312-321-4299
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-974-775-10
Query Match 1.4%; Score 6; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 424 NHEATS 429
DB 8 NHEATS 13

TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
CITY: Chicago
STATE: Illinois
ZIP: 60611-5599
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-28

Query Match 1.4%; Score 6; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
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DB 5 NHEATS 10

RESULT 11
US-08-974-775-8
Sequence 8, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
ADDRESSEE: Walsh-Reitz, Margaret
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
CITY: Chicago
STATE: Illinois
ZIP: 60611-5599
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.

REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-8

Query Match 1.4%; Score 6; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
|||||
DB 8 NHEATS 13

RESULT 12
US-08-974-775-27
Sequence 27, Application US/08974775
Patent No. 6096706
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
ADDRESSEE: Walsh-Reitz, Margaret
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
CITY: Chicago
STATE: Illinois
ZIP: 60611-5599
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,775
FILING DATE: 20-NOV-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-775-27

Query Match 1.4%; Score 6; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 NHEATS 429
|||||
DB 5 NHEATS 10

IMMEDIATE SOURCE:
LIBRARY: P. suis DNA in Bacteriophage lambda-dash
CLONE: (Lambda)yfc33-37
US-08-215-805A-80

Query Match 1.6%; Score 7; DB 1; Length 934;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 VKAEDL 244
Db 62 VKAEDL 68

RESULT 5
US-08-542-003-6
Sequence 6, Application US/08542003
Patent No. 5864013
GENERAL INFORMATION:
APPLICANT: Goldberg, Edward B.
TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,003
FILING DATE: 13-OCT-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8471-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: 212-869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacteriophage T4
IMMEDIATE SOURCE:
CLONE: p37 amino acid
US-08-542-003-6

Query Match 1.6%; Score 7; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 QTIKGP 134
Db 861 QTIKGP 867

RESULT 6
US-08-322-760A-6
Sequence 6, Application US/08322760A
Patent No. 5877279
GENERAL INFORMATION:

APPLICANT: Goldberg, Edward B.
TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,760A
FILING DATE: 13-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8471-0003-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: 212-869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Bacteriophage T4
IMMEDIATE SOURCE:
CLONE: p37 amino acid
US-08-322-760A-6

Query Match 1.6%; Score 7; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 QTIKGP 134
Db 861 QTIKGP 867

RESULT 7
US-09-236-949-6
Sequence 6, Application US/09236949
Patent No. 6437112
GENERAL INFORMATION:
APPLICANT: Goldberg, Edward B.
TITLE OF INVENTION: MATERIALS FOR THE PRODUCTION OF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,949
FILING DATE: 25-Jan-1999

RESULT 2
US-08-231-729B-6
Sequence 6, Application US/08231729B
Patent No. 5618722
GENERAL INFORMATION:
APPLICANT: ZENNO, Shuhel
APPLICANT: SHIRASHI, Shinji
APPLICANT: INOUE, Satoshi
APPLICANT: SAIGO, Kaoru
TITLE OF INVENTION: FIREFLY LUCIFERASE GENE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER
STREET: 700 Thirteenth Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,729B
FILING DATE: 20-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 119050/1993
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rose, Herbert C.
REGISTRATION NUMBER: 29846
REFERENCE/DOCKET NUMBER: 60130/No. 5618722aka
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-6770
TELEFAX: 202-737-6776
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-231-729B-6
Query Match 1.6%; Score 7; DB 1; Length 552;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 LSFIDL 181
DB 184 LSFIDL 190

RESULT 3
US-08-890-865A-4
Sequence 4, Application US/08890865A
Patent No. 6307019
GENERAL INFORMATION:
APPLICANT: Constantini, Franklin
APPLICANT: Zeng, Li
TITLE OF INVENTION: AXIN GENE AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,865A
FILING DATE: 10-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/54249
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-890-865A-4
Query Match 1.6%; Score 7; DB 4; Length 900;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 GKISGY 409
DB 268 GKISGY 274

RESULT 4
US-08-215-805A-80
Sequence 80, Application US/08215805A
Patent No. 5559008
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURILLA
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,805A
FILING DATE: 22-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 934 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Pasteurella suis
STRAIN: 5943

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 11:42:46 ; Search time 11 Seconds
(Without alignments)
1182.267 Million cell updates/sec

Title: US-09-787-083-8

Perfect score: 442

Sequence: 1 MKVSLSTLTLILPCFAILA.....YNHEATSFVGLMLNDMMGL 442

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	7	1.6	552	1	US-08-231-7298-6
3	7	1.6	900	1	US-08-890-865A-4
4	7	1.6	934	1	US-08-215-805A-80
5	7	1.6	1026	2	US-08-542-003-6
6	7	1.6	1026	2	US-08-332-760A-6
7	7	1.6	1026	4	US-09-236-949-6
8	6	1.4	10	3	US-08-974-775-30
9	6	1.4	11	3	US-08-974-775-29
10	6	1.4	12	3	US-08-974-775-28
11	6	1.4	13	3	US-08-974-775-8
12	6	1.4	13	3	US-08-974-775-27
13	6	1.4	14	3	US-08-974-775-9
14	6	1.4	14	3	US-08-974-775-10
15	6	1.4	15	3	US-08-974-775-32
16	6	1.4	16	3	US-08-974-775-4
17	6	1.4	16	3	US-08-974-775-5
18	6	1.4	20	1	US-08-430-273-1
19	6	1.4	21	1	US-07-918-953-13
20	6	1.4	21	1	US-07-918-953-15
21	6	1.4	21	1	US-08-212-696-1
22	6	1.4	21	1	US-08-158-245-1
23	6	1.4	21	1	US-08-081-661-13
24	6	1.4	21	1	US-08-081-661-15
25	6	1.4	21	1	US-08-233-617-1
26	6	1.4	21	1	US-08-160-376A-1
27	6	1.4	21	1	US-08-304-070-1

28	6	1.4	21	1	US-08-285-661-1	Sequence 1, Appl1
29	6	1.4	21	1	US-08-301-838-1	Sequence 1, Appl1
30	6	1.4	21	1	US-08-389-487-4	Sequence 4, Appl1
31	6	1.4	21	1	US-08-389-487-12	Sequence 12, Appl1
32	6	1.4	21	1	US-08-507-124-2	Sequence 2, Appl1
33	6	1.4	21	1	US-08-507-124-3	Sequence 3, Appl1
34	6	1.4	21	1	US-08-342-931-1	Sequence 1, Appl1
35	6	1.4	21	1	US-08-400-256-1	Sequence 1, Appl1
36	6	1.4	21	2	US-08-508-664-9	Sequence 85, Appl1
37	6	1.4	21	2	US-08-353-476-85	Sequence 87, Appl1
38	6	1.4	21	2	US-08-484-219-1	Sequence 1, Appl1
39	6	1.4	21	2	US-08-979-587-1	Sequence 1, Appl1
40	6	1.4	21	2	US-08-992-676-1	Sequence 1, Appl1
41	6	1.4	21	2	US-08-992-676-6	Sequence 6, Appl1
42	6	1.4	21	2	US-09-134-836-1	Sequence 7, Appl1
43	6	1.4	21	2	US-09-134-836-7	Sequence 2, Appl1
44	6	1.4	21	3	US-08-967-867-2	Sequence 2, Appl1
45	6	1.4	21	3	US-08-967-867-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-07-942-245-98
; Sequence 98, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-98

Query Match 1.68; Score 7; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

QY 387 PRSGKA 393
|||||
Db 4 PRSGKA 10